

FIGURE 1

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCATGGCGTCCCCGTCTCGGAGAC
TGCAGACTAAACCAGTCATTACTTGTTCAGAGCGTTCTGCTAATCTACACTTTTATTTTC
TGGATCACTGGCGTTATCCTTCTTGCAAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG
TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA
AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTTGGTTCGAAGTGGTCGCTGCCATCGTAGG
ATTTGTTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTGTCAT
TGTGTGGTGTCAACGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT
TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
ATTTCCCTTTGGAGTTGCTTGCTTCCAACTGATTGGAATCTTCTCGCCTACTGCCWCCTCTCG
TGCCATAACAAATAACCAAGTATGAGATAGTGTAACCAATGTATCTGTGGGCCTATTCTCTCT
CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAAGTTGCTTGGCTGGAGAACTG
ACAACACTACTTACTGATAGACCAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTCTGTTAGATCG
TTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAATGAAGT

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FIGURE 2

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGVSLNYSLLNEKATNVPF
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGVFVRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV
```

Important features of the protein:

Signal peptide:

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA
 GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGCTGGGCCCGGGAGGTAGAGAAAGTCAGT
 GCCACAGCCCCACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
 TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
 GCCGGGGTAGGCTCTGGAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTTAGAAGAGGGT
 GTTCCTCTTTTCGGGGTCTCACCAGAAGAGGTTCTTGGGGTTCGCCCTTCTGAGGAGGCT
 GCGGCTAACAGGGCCAGAACTGCCATTGGATGTCCAGAATCCCTGTAGTTGATAATGTTG
 GGAATAAGCTCTGCAACTTTCTTTGGCATTGAGTTGTTAAAAACAAATAGGATGCAAATTCC
 TCAACTCCAGGTTATGAAAACAGTACTTGGAAACTGAAACTACCTAAATGATCGTCTTTG
 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGCCAGGGTCTGTTGTTGACTCTCGAAGAG
 CACATAGCCCACTTCTTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG
 CCGAGATGACAGTGGAACAGATGACAGTGTGACACCCAACAGCAACAGGCCGAGAACAGTG
 CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTTCGGCCACCAAGGAGGGGC
 CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTGACACACT
 GGCAGTAATACGGACTCTTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
 GAAAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
 CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
 TGATAAGATTTGATGTTTTTGTGCTGCTGTCATCTACTTTGCTCGGAAATGTCTAAATGTTTC
 TGTAGCAGAAAAACGATAAAGCTATGATCTTTATTAGAG

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FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNV DGLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

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FIGURE 5

GGCACGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTAGCCCATTTGGCC
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCTTAACGGACTG
CAAGATGGAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
CAGGTGCCTGGGGCATGCAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC
CTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTCCCCTTCTACTTCCACATCTC
CATGGGCTGTGCCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCTCTGAGCCTTACGCTGGCCACTGTCAAC
GCCCCTGGCTGGAACCCCGCACACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC
TCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA
AATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA
AAAAAAAAAAAA

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FIGURE 6

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

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 GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQTVEKER
 GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

AATTCAGATTTTAAAGCCATTCTGCAGTGGAATTTTCATGAAGTAGCAAGAGGACACCATCTT
 CTTGTATTATACAAGAAAGGAGTGACCTATCACACACAGGGGAAAAATGCTCTTTTGGGT
 GCTAGGCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAACTAAAGATTGAAG
 ACATCACTGATAAGTACATTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCC
 AGAAGCTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCTGTCTGACTGAATCAGGATCAAC
 AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG
 AGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGT
 CTGATCAATAATGTGGTGTCCCGGCGTGTGGCTCCCAGTCTGACTGGCTGACACTAGAGGA
 CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC
 CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTGGAGGTGCGCTTGCA
 ATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGAAGGTTTCAATGACAGCTTAAG
 ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACAGGATTGTTCAAAACAA
 ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA
 GACATCAACAACAATATGGAGAAGGTTACATTGAAAAAGTCTAGACAACTGAAAGGCAA
 TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA
 GTCTCTTCCCTAAGACTCATTATGCGCTGGAAGATGCCAAATTTTCTGGATACCTCTG
 TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
 TCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT
 TTCAAGAACACATCTCCTTTTCAACCCCATTCCTATCTGCTCCAACCTGGACTCATTAGGA
 TCGTGCTTATTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGTCCCTG
 CTCGAAGTTTTCTTTGAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCTGCCCTGT
 ATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAATTGAAAGACTTGCCCATTCAAAATG
 ATCTTTACCGTGGCCTGCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGGAATGTT
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 AAAAAAAAAAAAAAAAAA

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FIGURE 8

```
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><subunit 1 of 1, 319 aa, 1 stop .
><MW: 35227, pI: 8.97, NX(S/T): 3
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LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCIEPGLFKNLADPVKVEKKLAIWEQLSPDIKQQYGEYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

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FIGURE 9

GCGGGCTGTTGACGGCGCTGCGGATGGGCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
 CCTCTCAGTCGGAGTTCTCTGACGCCGCCAGTGGGCGGGGCCCCCTTGGGCGCTCGCCACCCT
 GTAGTCATGATCCACCGCCGCGCCGCTCATCGGAGCTTCATCTCGGTGACGCTGAG
 CTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGCGGCGCTCGTGCTGGAGGAATGGA
 AGCAACTGTCGAGATTGACGCGGAATATGATTCTCTCTCTCTGCTTCTGCTTTTCTGT
 GGACTCCTCTTCTACATCAACTTGGCTGACCATTTGGAAGAGCTCTGGCTTTCAGGCTAGAGGA
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTAAAAACCAGCAAAATCCACCCGCTCTTACCAG
 CTCCTCAGAAGGCGGACCCGACCCTGAGAACTTACCTGAGATTTCGTACAGAAAGACACAA
 AGACACATCCAGCGGGGACCCTCACCTGCAGATTAGACCCCAAGCCAAAGACCTGAAGGA
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 ATCCGACAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGGCTGAGCAGGGCACCAG
 CTCCCTTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCCCTGCCACCGGCCAGGACACAGGG
 CACACCAGTGCATCTGAACTATCGCCAGAAGGGCGTGATTGACGCTTCTCTGCATGCATGGA
 AAGGATACCGCAAGTTTTCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCCTTCAGT
 GAGTGGTTTGGCGCTCGGCTCTCACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT
 GAGGAAGAATAATTGAGGAAGCCAGGAAGTGGGTGTCTGAAGAAGTTACACTTTGAAAAGGACG
 TGGAGCTCAACCTGTTTTCAGAGCAGATCCGCTCCTGGGGGGGCTCCTGAGTGCCTACCAC
 CTGCTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTGTGGAATCCGGCTAATGCTGCT
 TTTCAGAACACCATCCAAGATTCTTACTCGGATGTGAACATCGGATCTGGAGTTGCCACCC
 CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTCAGCTGGAGTTCCGG
 GAGCTCTCCGCTCTCACAGGGGATAAGAAGTTTCAGGAGGCATGGAGAAGGTGACACAGTA
 CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATACCCACAGTG
 GCCTCTTCACCACCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGTGGAGACCTACGTGGA
 AGCCATCGAGGGTGTGAGAACGCACCTGCTGCGGCACTCCGAGCCCAAGTAAAGCTACCTTTT
 TGGGGGAGCTTGCCACGGCCGCTTCAAGTGCCAAGATGGACCACTGGTGCTTCTGCCA
 GGGACGCTGGCTCTGGGCGTCTACACGGCCTGCCCGCCAGCCACATGGAGCTGCGCCAGGA
 GCTCATGGAGACTTGTTCACAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG
 TGCACCTTCAACCTTACCCCGAGCCGGGCGCTCGGGACGTGGAGGTCAAGCCAGCAGACAGG
 CACAACCTGCTCGCGCCACAGACCGCTGGAGAGCCTGTTCTACCTGTACCGCGCTCACAGGGGA
 CCGCAAAATACCGAGCTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTACACAGGGTCC
 CCTCGGGTGGCTATTCTTCCATCAACAATGTCCAGGATCCTCAGAAGCCCGAGCCCTAGGGAC
 AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTCTCTCTCCGATGA
 CCCAAACCTGCTCAGCCTGGACGCTACGTGTTCAACACCCGACCCTCTGCGCATATCT
 GGAACCTTGGCTAGGGTGGATTGGCTGCTGGTGTTGGGGACTTCGGGTGGGCAGAGGCACCTTG
 CTGGGTCTGTGGCATTTCACAGGGCCACGTAGCACCGGCAACCGCCAAGTGGGCCAGGCT
 CTGAACTGGCTCTGGGCTCCTCTGCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGA
 GGCGCTCAGTCTTGGTGTGATGCGGGGTGGGCTGGGCGCTGGAGCCTCCGCTCTGCTCTCT
 CAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCCGACCA
 GAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGTGACCGAGTGGACAGCCAGGGTGCAGC
 TCTGCCCGGGCTCGTGAAGCCTCAGATGTCCCCAATCCAAGGGTCTGGAGGGGGTCCGGTGA
 CTCAGAGGCTGAGGCTCAGGGGCTGGCTCTGGTGTTCAGAAGCTGAGCTCAGGATCCTCT
 CTGGCCGCCCGCAGGGGGCTTGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGCCCCCT
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FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529

><subunit 1 of 1, 699 aa, 1 stop

><MW: 79553, pI: 7.83, NX(S/T): 0

MAACEGRRSGALGSSQSDFLTTPVGGAPWAVATTVMYPPPPPPPHRDFISVTLSFGESYDN
SKSWRRRRCWRKWKQLSRLQRNMILFLLAFLLCGLLFYINLADHWKALAFRLEEEQKMRPE
IAGLKPANPVLPAFAQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGQTQEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTLPSSRAEVPTKPPPLPPARTQGTTPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRFSFSEWFGGLTLIDALDTMWILGRKEFEEA
RKWVSKKLHFEKDVDVNLFEFSTIRILGGLLSAYHLSGDSLFRLKAEDFGNRLMPAFRTPSKI
PYSDVNIGTGVAHPPRWTSDDSTVAEVTSTQLEFRELSTLTGDKKFQEAWEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTLGRADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLTFTVGELAHGRFSAKMDHLVCFPLPTLALGVYHGLPASHMELAEQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLRPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFRTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD
AYVFNTAEHPLPIWTPA

Important features of the protein:**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

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FIGURE 11

GGC GCCGCTAGGCCCGGGAGGCCGGCCGGCTGCGAGCGCCTGCCCCATGCGCCGC
 CGCTCTCCGCACCA**ATGTT**TCCCTCGCGGAGGAAAGCGCGCAGCTGCCCTGGGAGGACGGC
 AGGTCCGGGTGCTCTCCGCGGCCTCCCTCGGAAGTGTTCCGCTTTCACCTGTTCTGTGGC
 CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
 CCGGGCAGTCAAGGGACAAGGGCAGGAGACCTCGGGCCCTCCCGTGCTGCCCCCAGAG
 CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCCTGGCAGTGCTGGT
 GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCTCTGA
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 GCACGACGTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC
 CTTCCACGTGGCTCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTGCGCGGC
 ATCCTGTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG
 CTGGGGCCGCGAGGACGACGAGTTCTACCGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCC
 GCCCCTCGGGAATCACAACCTGGGTACAAGACATTTTCGCCACCTGCATGACCCAGCCTGGCGG
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 AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCC
 CCTGCACTGTCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCTGGTGCACATTC
 AGC**TGA**AGCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA
 CAAGGCCTCAGTCTGTGGGCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
 AGCTACGCAATTGCAGCCACCCGGCCGCCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG
 GTGCCTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCG
 GGACCCCCCTGCCTTCTTGCTCACCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGG
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FIGURE 12

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GQGQETSGPPRACPPPEPPPEHWEEDASWGPHRLAVLVPPFRERFEELLVFVPHMRFLSRKKI
RHHIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDDLPLNEELDYGFPEAGPFHVA
SPELHPLYHYKTYVGGIILLSSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRRKRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

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FIGURE 13

CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCT
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT
GGGGATGGC**TAA**GAAAGCTGGGAGATAGGGAACAGAAAGAGGGTAGTGGGTGGGCTAGGGGG
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC
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FIGURE 14

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

<MW: 7879, pI: 7.21, NX(S/T): 0

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PRGEGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 15

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAG
 GAGCATGTCGCCGCCGGGGAAGGCCCTCCTCCGGCCGCCATAAGGCTCCGGTCGCCGCTGG
 GCCCGCGCTCCGCGCTCTCGCCGCCGGGCTCCGGGCGGCCGCTAGGCCAGTGCGCCGCC
 CTCGCCCCGAGGCCCGGCCCGCAGC**ATGG**GAGCCACCCGGAGCCGGCGGGGCCGCCGCA
 GCCGCCGCTGTTGCTCGCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCCGCCGCCG
 GCGCGCGCCGCCGCCGCTGCCGCCGGCTGCAAGCACGATGGCGGCCCGCCGAGGGGCTGGC
 AGGGCGGCCGCCGCCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACCTCGCGCAGGTCTCT
 CCCCCAGATACTCTGCCAACCCGACGGTCACCCTGATTCTGAGTAACAATAAGATATCCG
 AGCTGAAGAATGGCTCATTCTCTGGGTTAAGTCTCCTTGAAGATTGGACCTCCGAAACAAT
 CTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTCATCTCTAAAAAGATTGGATCT
 GACAAACAATCGAATAGGATGCTGAATGCAGACATATTTCGAGGACTACCAATCTGGTTT
 GGCTAAACCTTTTCGGGGAATTTGTTTTCTTATTATCTCAAGGAACCTTTTGATTATCTTGGC
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 CACTGCAGGCCCAACAGTCACAGGCGTGAAGCAGGAGCTGTTGACATGCGACCCCTCCGCTT
 GAATTCGCGTCTTTCTACATGACTCCATCTCATCGCAAAGTTGTGTTTGAAGACAGACCTT
 TCCTTTCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTTGTGGTATCAGGATG
 GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTGTGTAAGAACATGATTCACACA
 TGCTCCTTGAATTGCAAGTGCCCTAACCAATTCTAATATTCAAGCTGGATCTACTGGAATTTG
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 CCCAGAACATTGGCAGGCATTACTGCATATCTGCAGTGTACGGGAACACCCATGGCAGTGG
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 TTGAAAAATTTGGAAGATTTACCAAGGAGGAAAAATCAAAGAGACTAGGTGACGTGATGGTT
 GACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCGCAGAGGGAAGC
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 GAGCTCACGTTTTATTCAACATATTACCCCAATATTGCTCTGGAAGCTTATGTCATCAAGTCT
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 ACTTTCGGATTATGGGAGCGGGATCCAGAGGGAACCTGGATAAGCAGCTGAGCTTTAAGT
 GCAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATTT
 AAGACTATTTCAGATT**TAA**ATTAGAATGTCTCCAAATGTTCTGCTTCGCAAAAATAACCTTATTA
 AAAGATTTTTTTTGCAGGAAGATAGGTATTATTGCTTTTGCTACTGTTTTAAAGAAAACCTA
 ACCAGGAAGACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTGGCCTTTGATTCCCTTT
 CTTCCACATAAAATATCAGAAATTACATTTTATAACTGCAGTGGTATAAATGCAATATACT
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 GCCTGCCAAGCCTAGTGGAGAAGTCAACCTGAGACCAGGTGTTAATCAAGCAAGCTGTAT
 ATCAAAATTTTTGGCAGAAAACACAAATATGTCATATATCTTTTTTTAAAAAAGTATTTCA
 TTGAAGCAAGCAAAATGAAAGCATTTTTACTGATTTTTTAAATTTGGTCTTTGATATATTT
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 TTTTCACTTAGCTTTCTGTGGGCATGTGAATTGTATTCTGCGGTTTTTAAATCTCACAG
 TACTTTATTTCTGTCTGTGCCCTCAATAATATCACAACAATATTCAGTCTATTTTAAATGGC
 TGCATAATACTGATCCAACAGGTGTTAGGTGTTCTGGTTTAGTGTGAGCACTCAATAAATA
 TTGAATGAATGACGAAAAAAGAAAAA

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FIGURE 16

MEPPGRRRGRAQPPLLLPLSLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
 VVCSSLELAQVLPDPTLPNRTVTILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
 FWGLSSSLKRLDLTNNRIGCLNADIFRGLTNLVRNLNSGNLFSSLSQGTFDYLASLRSLFQT
 EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPLLELPSFYMTP
 SHRQVVFEGLSLPFQCMASYIDQDMQVLWYQDGRIVETDESQGFVEKNMIHNCSLIASALT
 ISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPEVVNNKGDFRWPTLAGITA
 YLQCTRNTHSGSIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMFNL
 TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVMDIASNIMLA
 DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
 VFQKVAASDRTGLSDYGRDPEGNLDKQLSFKCNVSNTFSSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
 433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
 384-390, 403-409, 554-560

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FIGURE 17

GCGTGGGG**ATG**TCTAGGAGCTCGAAGGTGGTGTGGGCCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCCAAATTCGGAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAAA
TCAT**TGA**CTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTGAT
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTTTTGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

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FIGURE 18

MSRSSKVVVLGLSVLLTAATVAGVHVKKQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:

amino acids 1-21

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FIGURE 19

CTGTCGTCTTTGCTTCAGCCGCAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTC
 CAAGTGTGGCTTAATCCGCTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACC
 GCTGCCATGCCAGTGACGGTAACCCGCACCACCATCACAAACCACCACGACGTATCTTCGGG
 CCTGGGGTCCCCATGATCGTGGGGTCCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTTCGC
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC
 GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGTCTCTGCTTCTCCGTGACCCTGATCA
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC
 ATCACCTTCGCCTGCTATGCGGGCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCACCAC
 CTATGTCCAGTTCTCTGTCCCACGGCCGTTCGCGGGACACGCCATCGCCGCCACCTTCTTCT
 CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGCGCCGGCCGGCGAG
 ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGTGCTGGAGACCTTCGTTGCCTG
 CATCATCTTCGCGTTTCATCAGCGACCCCACTGTACACGACAGCCGCGCCCTGGAGTGGT
 GCGTGGCGGTGTACGCCATCTGCTTATCCTAGCGGCCATCGCCATCTGTCTGAACCTGGGG
 GAGTGCACCAACGTGTACCCATCCCCCTTCCCCAGCTTCTGTGCGGGCTGGCCTTGCTGTC
 TGTCTCTCTATGCCACCGCCCTTGTTCTCTGGCCCCCTTACCAGTTCGATGAGAAGTATG
 GCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGAGCCATGCCTACTACGTGTGT
 GCCTGGGACCGCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC
 TGACCTGGTGCACCTCTGCCACCTGGTTTTTGTCAAGGTCTTAAGACTCTCCAAGAGGCTCC
 CGTTCCTCTCCAACCTCTTTGTTCTTCTTGCCCCAGTTTTCTTTATGGAGTACTTCTTTCC
 TCCGCCCTTCTCTGTTTTCTCTTCTCTGTCTCCCTCCCTCCCACCTTTTTCTTCTCTTCC
 CAATTCCTTGCACTCTAACCAGTTCTTGATGCATCTTCTCTCTTCCCTTCTCTTCTGTGT
 TTCTCTCTGTGTGTGTGTGTGTTGCCACATCCTGTTTTACCCCTGAGCTGTTTCTCTTTT
 CTTTTCTTCTTTTTTTTTTTTTTTTTTAAGACGGATTCTCACTGTGCGCCAGGCTGGAG
 TGCAGTGGTGCGATCTCAGCTCAGTGAACCCCGCCTCCTGGGTCAAGCGATTCTCTCTCC
 CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTTCTCTT
 TTCCACTCTTCTTTTTTCTCATCTCTTTTCTGGGTGCCTGTGCGCTTCTTATCTGCCTGT
 TTTGCAAGCACCTTCTCTGTGTCTTGGGAGCCCTGAGACTTCTTCTCTCTTGCCTCCA
 CCCACCTCCAAAGGTGTGAGCTCACATCCACACCCCTTGAGCCGTCATGCCACAGCCCC
 CCAAGGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC
 GTGTGTGTGTGTGTGTGTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTTTTCT
 CCCAGTGGAGGAAGGTGTGCAGTGTACTTCCCCCTTAAATTAAAAAACATATATATATAT
 ATTTGGAGGTACAGTAATTTCCAATGGGCGGGAGGCATTAGCACCGACCCTGGGTCCCTAGG
 CCCCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGCCAGGCTTACAGAACAC
 CCACTGCCTAGAGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCATCCCAACTATTCT
 CTGTGGTATGAAAAAG

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FIGURE 20

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLIILIVELCGLQARFPLSWRNFPIITFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAIATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNLGECTNVLPPIPFPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFVKV
```

Important features:

Transmembrane domains:

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192, 205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

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FIGURE 21

GAACGTGCCACCATTGCCAGCTAATTTTGTATTTTATAGAGACGGGGTTCCACCATTGTGGCCAGGCTGGTC
 TTGAACCTGCTGACCTCATGATCCGCTCACCTCGGCCCTCCCAAGTGCTGGGATTACAGGCATGAGGCACGTGAGCC
 CTGGCCAGCCTAGCTATTTTAAAGAAATTTATCTGTATTAGGTGCTGCTAAACATTGGGCATCATACAGTGACCA
 AAACAGACTGAATTCGCCAAGAGCCAAAGACCAGTGAAGGAGACCAACAAGAAACAGGAATGCAAAAGAGACCA
 TTATTACTCATATGACTAAGGTCACAAATGGGGTACGTTGATGGAGAGTGATTTTAAAGAGACTACAGAGGG
 AGGACAGACTACCAAGAGGGGGGCCAGGAAAGCTCTCTGACGAGGTTGGTATTTCAGCCCAAATCGGAAAGATGA
 GAAGAGCTAGCCAGCATCAGAATAGTCCAGAAGAGATGGGGAGCACTACACTCACTACACTTTGGCCTGAGAA
 AATAGCATGGGATTGGAGGAGGCTGGGGGAACACCCTTCTGCCGACCTGGGAGGAGGCATTGAGGGCTTGAGA
 AAGGGCAATGGCAGTAGCAGTAGAAGGACAGGGTAGGAGCAGGGACTTTGCAGGTGGAATCATTAGGCTTTATC
 AACAGATATGGCAAGCAAGCCAGGGAGGAATGATGGTAATGCTGAGGTTTGGAGCCAGGCTAGATGGGACAG
 TGGTGGGTGATGCAAGGAAAGAGGTGAGGAAGCAGGGCCAGAGCTGGGAGAGAGGTGTGGGGGTTTGGTTTCCA
 TCTTGCCGAGTCTGCCGGAATGTGGATGGGAAGACCAAGAGGAGGAGCAAGGGGCGAGAGGGGAAAGGAATCTTAA
 AGAAGTCTGGATGCCACACTCTTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 TTCTGCTGCTGCTCCATCTCTCTGGGTGCTGGGAAATGGAGGATTAGCTGAAGTTTGTCTCTCGGGCCCTG
 TCTGAATCTCCATTGCTTCTGGGAGGACATAATCACCTGTCTAGCTTCTTATCATCTTACATTTCCCTGTAG
 CCACTGGGACATATGTGGTGTCTTCTTCTAGCTCCTGTCTCTCTCATGCCCTTGTCTGGGTATGGGCATGTAG
 GGGGAAGGTCTTGTCTGACAGGGGCACTGACTTCTTAATGGTGTACCAAGGTGAATGTGGAGACACAGT
 CGCATGCTGCCCAAGTCCGGCGGACCCCTAACTATCAGGAGATCGCTGCGCTGGCCAGGTCTCTCCCTGCATGCT
 ATCAGCCTCCCTCCATGTTTCTGGCCACTTTGTCTTCTCTCCCGTTTGCATCACTCTTGGAACTGTTTCTCT
 GTGAGTACATGCTGGGTCTCCCTTCTTCTTCTGCTCAGGTGAATCTCAGCCCTTCTCCCAACCAAGGTTTC
 ACATGGATCCTAACTAGCTGCCACCTTCCACCTCCCTGCACTGTGCTCCCTGCTGCTCTTACCAGGCTTC
 TCCACCTCCCTATCTCCAGGTATTTCCACAGTGGTGAAGGACCAGCTGACCAAGCTTACCGCCATGGCCACAGG
 GCCGATGGCTCACTCATTTAGTGGAAAGGGCTGGAGCAAGCCGAGTGACTCACTTGGCCCTGGAATCAGCTT
 TTTCTCTCTATTCAGACTCAGCGAGGGCGAACAAGAGGCTCGCTTTGACAGCAGGAGGGCTGAGCAGTTTGCCA
 TCGCGGAAGCCAAAGCTCCGAGCATGGTCTTCGGTGGATGGCGAGGACTCCAATGATGACTCTTATGATGAGGACT
 TTGCTGGGGAATGGACAGACATGGCTGGCGAGCTGCCCTGGGGCCGCACTTCAGGACCTGTTCACCGGCC
 ACCGGTTCTCCCGGCTGTGCGCCAGGGCTCCGTGGAGCCTGAGAGCGACTGCTCACAGACCTGTGCTCCGACGA
 CCGTGTGCTCTAGTCTGTGACGCTGGAGGATGGGTGTTGGGCTCCCGGGCCGGCTGGCTCCCAAGCTGTGG
 GCGATGAGCTGCTTCTGCCAAACTGCCCCAGCCGGGAAAGTGCCCTCCGACAGTGTGGGCCATGTACGAGGCTC
 AGGACTCACTTACAACCTGCCCTCAGAGAGTCTGCTTCTCCCGCGGAGGAGGAGGAGCCAGCCCTTCAAGG
 ACTGCCAGCCACTCTGCCACCACTAACGGGCACTGGGAACGGCAGCGGCAAGCTCTGACCTGGGCTTCTGT
 GGGTGGTGTCTTAGATGAGGATGAGGCAGAGCCAGAGGAACAGTGAACCACTATCGCTGGCAGTGGCATGCA
 TGCCCCGGCTGCTGCCAGGGCAGAGCCTCTGTGGCCAAAGTTGGGCTCAAGGCTCCAGCAGAGCTCCACAGCC
 TAGAGGGCTCCTGGGAGGCTCGCTTCTCCGTTGTGTGTTTGTGATGAAAGTGTTGGAGAGAGGCGGGGCTG
 GGCTGGGGGCGCATGCTCGCCGCCACTCCCGGGGCTTGGCGGGGCTTGGCGGGGCTCTGGGGCATGGCTACA
 GCTGTGGCAGACAGTGATGTCTGATGTTCTTAAATGCCACACACATCTTCTCTCGGATATGTGAACCACTA
 AGGGGGTTGTGACTGGGCTGTGTGAGGTGGGTGGGGGGGGGCCAGCAACCCCACTCCCTCATGCTCTCTC
 TCTCTCTGCTTTTCTTCTCACTTCCGAGTCCATGTGCAGTGCTTGATAGAATCACCCCACTCTGGAGGGGCTGG
 CTCCTGCCCTCCGGAGCGCTATGGGTTGAGCCGTCCTCAAGGGCCCTCCGACCTGGGCTGCTGCTGTGCTCT
 ATTCACTTCTCCATGCTCTCTAAATCTTCTCTTTTTCTTAAAGACAGCAAGGTTTGTGCTGTGTTTTCAGTC
 GGAATCTCTCTCTCTGAGGACTTTGGAATGATGAAAGCATGTACCTCAACCTTTTCTCGGCCCATATAGG
 GGCTCGGGCCCTTCCCAACCCCTCCTAGGATGTGCGGGCAGTGTCTGGGCGCTCACAGCCAGCGGGCTGCC
 ATTCAGGAGGCGCCACAGAGGGGCCACAGGGGTGGCGGAGTGTGCTGCTGCTGCTGAGAGCGAGGAAT
 TGTGCGACTGAGTGACAGTCAAGGAGTGTCTCTTCTGGGAGGAGGAGGAGTGAAGGCTTCTGCTGTGAAT
 GAAAGGCCAAGGCTACAGTACAGGGCCCGGCCAGCCAGGCTGTTAATGCCACGTAGTGGAGGCTCTGGCAG
 ATCCTGATTTCAAGGTCACTGGACTGTACGTTTATGGTTTGGGAAGGGTGGGTGGCTTGAATTAAGGCG
 CTTGTAGGCTTTGGCAGGTAAGAGGGCCCAAGGTAAGAACGAGAGCCAACGGCCACAGCATCTATATTAAGT
 GGCTCAATAGGTGTTTATTTGTTCTATTAAAGATTTGTTTATTAATTAATATAAAATCTTTGTAATCTC
 TAAA

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FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSP LSSLAQVNLSPFSPKPVHMDPNYCHPSTSLHLC
 LAWSFTRL LHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALES
 AFSSY
 SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYEDDFAGGMDTDMAGQLPLG
 PHLQDLFTGHRFSRPVRQGSVEFESDCSQTVSPDTLCSSLC SLEDGLLGSPARLASQLLGDE
 LLLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTG
 SWER
 QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
 285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTTCCTGGGCGCTCTGTTCACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCTT
 GGCACCTCCTGCTCAGTGCACATTGTCACACTTAACCCATCTGTTTCTCTAATGCACGA
 CAGATTCCTTTACAGACAGGACAACCTGTGATATTCAGTTCCTGATTGTAAATACCTCCTAAG
 CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA
 TACAATCTATTCTTGCCACATCAAGGGATTGTTATTCTTTAAAAAAAACCAATACCAAAG
 AAGCCTACAA**ATG**CTTGGCCTTAGCCAAAATTCTGTTGATTTCACGTTGTTTTATTCACTTCT
 ATCGGGGAGCCATGGAAAAAGAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT
 TTAAACCAATGGAAATAAACCTATTCTTTGGAAAGTGAGCAAACTTAAACTCAGATAAA
 GAAATATAACCACTCAAATCTCAAGGCGAGTCATCCCTCCTTTGAATCTACCCAACAA
 CAGCCACGGAATAACAGATTTCTCCAGTAACATCAGCAGAGCATTCTTTGGGCAGTCTAA
 AACCACATCTACATTTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCTT
 TGGAATGCACCTATAGCAGATGAAGATCTTTGCCCATCTCAGCACATCCCAATGCTACACC
 TGCTCTGTCTTCAGAAACTTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCCTGATA
 ACAGTTCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG
 ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA
 TCAAGAAAAACAACCTCTACAGCCTACCTTAAATTCACCAATAATTCAAACCTCTTTCCAA
 ATACGTGAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTTAGGT
 GCTATTCTGGGTGTCTCATGTGCTTACTCTTGTGGGCTACTTGTGTGTGGAAGGAAAAAC
 GGATTCATTTTCCCATCGGCGACTTTATGACGACAGAAATGAACCAAGTTCTGCGATTAGACA
 ATGCACCGGAACCTTATGATGTGAGTTTGGGAATTCTAGCTACTACAATCCAACCTTGAAT
 GATTCAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATACC
 TCCACTTCGTACTTCTGTAT**AGA**ACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCATCTA
 CATCCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTACTGTCACGTGGAT
 TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
 CCAAAGGTTTTCTTTCTTACAATTTTGGCCATCCTGAGGCATTACTAAGTAGCCTTAATT
 TGTATTTTAGTAGTATTTTCTTAGTAGAAAATATTTGTGGAATCAGATAAACTAAAAGATT
 TCACCATTACAGCCCTGCCTCATAACTAAATAATAAAAATTATTCCACAAAAAATTCTAAA
 ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT
 TTTCTTAAATGAAAATTGAAAGGGTGCTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG
 GACATAGCCAGAGTTTCTGTTATTGGGAATTGAGGCAATAGAAATGACAGACCTGTATTTC
 TAGTACGTTATAATTTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA
 CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCTACCCAGGAAAGTAATAGCT
 TCTTTAAAGTCTTCAAAGGTTTTGGGAATTTAACTTGCTCTTAATATATCTTAGGCTTCAA
 TTATTTGGGTGCCTTAAAAACTCAATGAGAATCATGGT

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FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSSEFTWVSLVNDTVKTPDNSSITVSISSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFNTSDPQKENRNTGIVFGAILGAIL
GVSLTLVGYLLCGKRKTDSFSHRRLYDDRNEPVLRLDNAPEPYDVSVFGNSSYYNPRTLNSA
MPSEENARDGIPMDIPPLRTSV

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

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FIGURE 25

AACAGGATCTCCTCTTGCACTGTCAGCCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
AGCCCGAAGATTCACTATGGGTGAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG
AGGCGCGGCAAGACGTGGAGGCCCTCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
CTTAGGCCCTTTCATTTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT
TCATGCCCAAGAGACCATTTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA
AATTCCTTTCGTGGAGGAGAGCCTAATTCTCGCTGTGACTGAGGAGGCTGACATTCGTGA
GGATGACAACATTGCAATCATTGATGTGCTGTCCCCAGTTTCTCTGATAGTGACCCCTGACG
CAATTATTTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTGTCTGGGGAAGTGC
TATCTGATGCCCCCTCAATACTTCTATGTATTGCTCCAAAAAATCTGGTAGAGCTCTTTGG
CAAACCTGGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGGTTCGAGAAGACCTAGTTGCTG
TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA
AAGTCTTCCGCTTCGTGCGCAGAGACCTCTGTGGGTTTCAACAAACGTGCCATTGATAA
ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAGT
AAGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA
CATTAAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT
AAAAAAGGAAAAAAAAAAAAAATACTAACCCTGCAAGCTCTTGTCAAATTTTAGTTTAAT
TGGCATTGCTTGTTTTTTGAACTGAAATTACATGAGTTTCATTTTTCTTTGCATTTATAG
GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCATCC
GTTGTTTTTTTTGTTTGTGTTTTTCTTTTCTTTAAGTAAGCTCTTATTTCATCTTATG
GTGGAGCAATTTAAAAATTTGAAATATTTTAAATTGTTTTTGAACCTTTTGTGTAAAAATATA
TCAGATCTCAACATTGTTGGTTTCTTTTGTGTTTTTCATTTTGTACAACCTTCTTGAATTTAGA
AATTACATCTTTGCAGTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT
TTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTCTCACTACTATCTGTATTGTGG
AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATCTACAA
CCCTATAATAAATTTTACTCTATACAAAAA

FIGURE 26

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVTRTQILTGKELRVATQEKEGSSGRCLMTLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDSDPAAIHDFEKGMTAYLDDLLGNCYLMPLNTSIVMPPKNLVELFGKLAGS
RYLPQTYVVREDLVAVEEIRDVSNLGIFYQLCNNRKSFRLRRRDLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE
```

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

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FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCCAGCCCCAGAGCAGCCCCGGGCACACGAGCTCTCT
 CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTTCGGCGGGAGCACCAGTCTGTACGCC
 AAGGAACTGGTCTTGGGGGCACCATGCTTTTCGGCGGCAGCCCCAGCCTCCTCATCCTTCTG
 TTGCTGCTGCTGGGGTCTGTGCCTGTCTACCGACGCCCCGCTCTGTGCCCTGAAGGCCACGTT
 CCTGGAGGATGTGGCGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCCTCCCGAGCCTCC
 CGCCACCCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCCCAACCCCTGGGG
 GGCCCATCACCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGTGTATGTTTCATCGTCTGTGCCCGGGTCA
 TCACCCGGCAGAAAGCAGAAAGGCCTCGGCCATTACCCATCGTCTCTCCCAAGAAGAAGTAC
 TTGGACACAGAGTGACCGGGCGGGGGCCCCCGGGCCTTCAGTGAGGTCCCGACAGAGCCCC
 CGACAGCAGGCCCGAGGAAGCCCTGGATTCTTCCCGCAGCTCCAGGCCGACATCTTGGCCG
 CCACCCAGAACCCTCAAGTCCCCCACCAGGGCTGCATGGGCGGTGGGGACGGAGCCAGGATG
 GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGACAGGAAGTCCA
 GGGACATGGGGTCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTG
 AGGGGGCTGTGGTGGCCGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTTTGTTAGCCAG
 GAAGCCAGGGACAGTGGGTCCCCCGAAAGCCCTGTGCTTGCAGCAGTGTCACCCAG
 TGTCTAACAGTCTTCCGGGCTGCCAGCCCTGACTGTGCGGCCCCCAAGTGGTCACCTCCCC
 GTGTATGAAAGGCCTTCAGCCCTGACTGCTTCCTGACACTCCCTCCTTGGCCTCCCTGTGG
 TGCCAATCCCAGCATGTGCTGATTTCTACAGCAGGCAGAAATGCTGGTCCCGGTGCCCGGA
 GGAATCTTACCAAGTGCCATCATCTTCACCTCAGCAGCCCCAAAGGGCTACATCTTACAGC
 ACAGCTCCCCTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC
 CCCAAAGTGTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCAAACTACTTTTAAACA
 GCTACAGGGTAAATCTCTGCAGCACCACCTCTGGAAATACTGCTCTTAATTTTCTGAAG
 TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTAAATCCTC
 TCAAGCGCTCTCAAGCACCCCCGGCCTGGGGGTGAGTTTCTCATCCCGCTACTGTGCTGG
 GATCAGGTTGAATGAATGGAACCTTCTCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG
 GCTGTGTTTGAAGGGACCTCCACCCTGGGGAAGTCCGAGGGGTGGGGAAGGGTTTCTGACG
 CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTGCTCACACATTGTCTGGCAGCCTG
 TGTCCACAATATTTCGTAGTCTCTGACAGGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCT
 CTGGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT
 CCAGGTGCTGAGATATAATGCACCAGCACATAAACCTTTATTCCGGCCTGAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

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FIGURE 28

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAGSSASSPSLPPPTPAL
SPTSMGPQPTTLGGPSPTNFLDGIVDFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGFVGPPEPCACSSVHPSV
```

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

[illegible]

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FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGFLACLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAPWQGQGGNGGFPNFGTNTQGAVAPGYGVSVRASNQNEGCTNPPSGSGGGSSNSGGGS
GSQSGSSGSGSNGDNNNGSSSSGSSSSGSSSSGSSSGSSSGSSSGSSSGSSSGSSSGSS
GSSTGSSSGNHGSGGGNGHKPGCEKPGNEARGSGESGIQGRGQGVSSNMREISKEGNRL
GGSGDNYRGQGSWSGSGGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP
```

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 31

GACCGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCGCGGGCGGGTCTCACC
 TCGCCTGGCTGGTGGAGTTTCTCTCCTTTGCTGACCATGTTGTTCCCTTGTCTGGAATATTACCGGGACATCTTCA
 CTCTCTCTGCTCGCCTGCACCCGGAGCTTGGTGTGTCGAGGAGAGTGAGGGGAAGATGTGTTTCTTGAACAAGC
 TGCTGCTACTTGTCTGCTCGGGCTGGCTTTTCCAGATTCCACAGTCCCTGAGGACATGTTCTTTCTGGAAGAGG
 GTCCTCATATGCTTTGAGGTTGGACACAGTAGCCCGAGAGCATGGCTTGGACAATGCCCTGTGGTGGACCAAGC
 AGCTGCTTACACCTGCTGCCCTACATCGGAGAGCTCCGGAACATGCTCGTTTCGTGGGTGTACGGCAGTAGTG
 GACGGAGTGGGGCTTTCATGAGGAAATCACCCCCACCACTACCCAGCTGGGAGCCAGCCTTCCAGAGCA
 GCCAGGGGCTGCAGGCACAGCTCGCCAGGCCCTTTTCCACAACAGCCGCCCTCCTTGGCCGGACCGCTAGAGT
 TCGTGGCAGAAAGATTGGATCAAACTGTGTCAAACATATCAAGGCTACACTGGTGGCAGATCTGGTGGCCAGG
 CAGAGTCACTTCTCCAAGAGCAGCTGGTGACACAGGAGAGGAAGGGGGAGACCCAGCCAGCTGTTGGAGATCT
 TGTGTTCCAGCTGTGCCCTCACGGGGCCAGGCATTGGCCCTGGGGCGGGAGTTCGTCAAAGAGAGGCCCTG
 GGGCTGTGGGGCGCTGCTTCCAGAGGAGACCCCGGCAGCGTCTGAGCAGTGCAGAGAACATTGCTGTGGGGC
 TTGCAACAGAGAAAGCGTGTGCTTGGCTGTGAGCAACATCACAGCACTGATCAGGAGGGAGGTGAAGACAGCAG
 TGAGTCGCACACTTCAGGCCAGGGTCTGAACTGCTGCGGGGGGAGCGGAGGGGCTGCTCCCGCGCTGAC
 GTGCTCTCCTTGGCGCTGGGGCCACGGACCTTGACGAGGAGTCTCCCCAGAGCATCTGGAACAGCTCCTAGGC
 CAGCTGGGCCAGAGCTGCGGTGCCCGCAGTTCTGTGCCACCTGCTGAGCAGCATCTGGCAAAGTCTCTGTG
 GAGTTAGCTTCCCTCCTCGTTGCAGATCAAAATTCCTATCTTAGGGCCCGGGCAGCAGTACAGGCTGGAGAGGG
 CAGGCTCGAAGGCTTCTGCACATGCTGCTTCCCTTGTGAAGGAAGACTTTCAGGGGCGGGTCCGCTGCAGCTG
 CTGCTGAGCCCAAGAAATGTGGGGCTTGTGGCAGACACAAGGCCAAGGGATGGGACTTGTGCTATTCTTGCTA
 CGGGAGCTGGTGGAGAAGGCTGTGATGGGACGGATGGAGATAGAGGCTGCTTGGGACAGCTCCACAGGCCAG
 TGGCCAGGGGACTTGTCTGAAGAATTAGCAACACTGTCTAATCTGTTTCTAGCCGAGCCCACTGCCACGAACC
 CAGCTAAGAGCTTGTGAGTTGGTGAGCCAAACCGGGCACTGTGCTGGCCAGAGCTAGGCGTGAGAAGTGCC
 CTGCTTGGGCATTGCAACCAAGCCCTGGACCCCGCCCTCACGAGGAGGCCAAGTGGCCAAATGCAGACCTCA
 TGCTTGGGTGTAGCTGGGTCTACAGTCAGACTTCTGCTCTAAGGTTGTCACTGCTGCCATCCCAACAGCGGA
 ATCTTAGGGAAGAGAGACTTGGCGTATTGGGATTATGGCAGAAAGTCCAGAGATGGCAGTCTGGAGTCTGA
 GAGTGGTGTGTTGTTTATCTCTTGATATAAATGAATGAGGTGTGTGGGCTGTGCAACACAGAAATCAAGCT
 CATTTGCTATCCCACTCTCTTAAAACTTGTAGTCTTGAATCATGACACAGGCAATGACTCTGCTTAAC
 TTATGAAGAAAGTTAAACATGAATCTTGGGAGTCTACATTTTCTATCACAGGAGCTGGAATGCCATCTCCTT
 ATAAATGCCATAACACAGCCGGGTCTGGTGGCTCATGCTGTAATCCAGCACTTGTAGAGGCTGAGGCTCGCGG
 GACTGCTGAGGTGAGGAATTAAGACCAAGCTGGCCACATGGCAAAACCCCATCTCTACTAAAAATAAAAAA
 TTATTAGCTGGGCATGGTGTGTGTGCTGTAATCCAGCACTACTCAGGAGGTGAGGCGAGAGCACTGCTTGAAC
 CTGGAGGTGGAGGTGTCAGTGAGCCGAGGTGCGACCACTGCACTCCAGCTTGGGTACACAGAGAGAGACTTCTG
 AAAAAGCCTAACAAACAGATAGGTAGGACTCAACCAACTGAACTGAACTTTCCTTGTACCTTCAAGCCCTG
 TGCAGTGTGTAACCTTTGAGACCTCTCCCTGACCAAGGACCAAGCACAGGCACTTATAGAGCTTTTGAATAAA
 CTGTTTCTCTTTTAAAAAAGGGCTTTTATTAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
 TTTTCTTTTCTTTTAAAAAGGGCTTTTATTAATTTCTCCCCACAGATGGCTGCAATCTGCCACAGCTC
 TGGGGCGTGTCTGTGAGGAAGGCTGTTTCTTCCCTGAGGCGGGCTGGGCTGTCCATGGGTGGCGGAGCTG
 CGCGTGTGTGGCGCCTTGGCGTGTGTCTAGCTGCTTCTTGGCGGGCACAGAGTGCAGGCTTGGGGGACCGGG
 AGCTAAGACAGGCTCTGTGTGAGGGGTGAGGCGTGTCTCTTAACGCAACCTGAGGCTGCTCTGAGTGTCTG
 GTTCCACCTGAGTGGCACGGGAGCAGCTGTGGCGGTGCTCTCTTCTAGGCGAGCTTGGGGAATCAAGCTC
 GGCGCTCTCTTTTGAAGAAGCAGGATGGGTGGGTGTGGGGGACTCATGGGAATGGCTGAGGACTACGTGTG
 GAAGAGGCGCGGCTGTTTGGCTGCACGGGCTGGAGCGCTCTCTCTGAGCCTCAGTTTCCCTTCCGCTCTA
 ATGAAGAATCGCGCTCGGCTCTCAGGCTATTAGGACTTGCCTCAGGAAGTGGCCTTGGACAGGCTGCTAT
 GTTATTTCACACTGTCTGCGAGCTTGGCTGGGACGTCATGGAATGCCCATGTCCCTCTGCTGCGTGGAC
 CTGGCGTGGGAGTGGAGCAGAGGCGGGGCGAGAGTGGCGCTGGGGGTGGGGGAGGCGCGCCGCCAGCCGTC
 CCTCAGGAAGTTGGGCTCCCGACACCCAGGCGAGGCGGGCTCCGCGCGCGCGCCGCCACCCGTCAGG
 GGCGCTAGACAAGTGAAGTGGGCTTGGGCTGCTGCGCAGCACTGACCTTGTGATGAGTGGCGGACGGCG
 TCGTCCGCACTGGAAGCAGCGCCCTCCACAGCACGAACGCCGTTGCGCT

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FIGURE 32

MCFLNLLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPHEGLDNAPVVDQQLLYTC
CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP
SLRRTVEFVAERIGSNVCVHKIKATLVADLVRQAESLLQEQLVTQGEEGDPAQLEILCSQL
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL
IRREVKAAVSRTLRAQGPEPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGTCTGGTGGCTGGTTGCGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG
 AAGACTCTCTGCTTTTGCCACAGCAGTTCCTGCAGCTTCCTTGAGGTGTGAACCCACATCCC
 TGCCCCAGGGCCACTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAAATG
 AGTAGCAACAAGAGCAGCGGTGACAGTGTTCGTGATCCTCTTTGCCCTCATCACCATCCT
 CATCCTCTACAGCTCCAACAGTGCCAAATGAGGTCTTCCATTACGGCTCCTCGGGGGCCGTA
 GCCGCCGACCTGTCAACCTCAAGAAAGTGGAGCATCACTGACGGCTATGTCCCATTTCTCGGC
 AACAAGACACTGCCCTCTCGGTGCCACCAAGTGTGTGATTGTGACGAGCTCCAGCCACCTGCT
 GGGCACCAAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGTACAAATCCGCATGAATGATGCAC
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACCGCGCTGTGGGCCATTCC
 AGTGTGTTCCGCGTGCTGAGGAGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCCGTGTT
 CATCTTCTGGGGGCCCGGAGCAAGATGCAGAAGCCCCAGGCCCTCGTGCGTGTGATCC
 AGCGAGCGGGCCTGGTGTTCGCCAACATGGAAGCATATGCCGTCTCTCCCGGCCGATGCGG
 CAATTTGACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCGTGGTT
 GAGCACAGGCTGGTTTACCATGGTGATCGCGGTGGAGTTGTGTGACCAAGTGCATGCTATG
 GCATGGTCCCCCAACTACTGCAGCCAGCGGCCCGCCTCCAGCGCATGCCCTACCACTAC
 TACGAGCCCAAGGGGCCGACGAATGTGTACCTACATCCAGAAATGAGCACAGTCGCAAGGG
 CAACCACCAACCGCTTCATCACCGAGAAAAGGGTCTTCTCATCGTGGGCCACGCTGTATGGCA
 TCACCTTCTCCCAACCCCTCCTGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCTAG
 AGGAGAAGCAGCCTCCGCCAGCCCGTAGGCCAGGGACCATCTTGTGCCAATCAAGGCTTG
 CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCTCCAGCCAATCAGGGCC
 TGGGGAATCTGTTGGCGAATCAGGGAATTTGGGAGTCTATGTGGTTAATCAGGGGTGCTTTTC
 TTGTGACAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGTATTTCTGAGTCAATCTG
 AGGCTAAGGACATGTCTTTCCCATGAGGCCTTGTTTCAGAGCCCCAGGAATGGACCCCCCA
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTGCCAAGGAGTGGGAATCTGGTGTG
 CCCCCTCAATTTCCAGCACCAGAAAAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGCCCC
 GGCCAGAGAATTTGTGGGTTGTGGAGTTGTGGGGGGGTGGGAGGTCACAGAGGTGGGA
 GGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTGGACAAACCCCTCCCCCTCTGCGG
 CACCCTTCTGCCACACCAAGTTTCCAGTGCAGGCTGTGAGACCTTTCCACCTCCCCACAA
 GTGCCCTCGGGTCTGCTCCCCGTCTGGACCTCCAGCCACTATCCCTTGCTGGAAGGCT
 CAGCTCTTTGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAACCTTTAGGGTATTTTTCG
 GCAAACCTCTCAGGGTTGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT
 TAGCCCCCTCAGCCAGTGCCTATAGCTTGGCTCTTAAAGGGCCAGGCCTCCTTTCTGCCCC
 CTAGCAGGGAGGTTTTCCAACCTGTTGGAGGCGCCTTTGGGGCTGCCCTTTGTCTGGAGTCA
 CTGGGGGGTTCCGAGGGTCTCCCTCGACCTCTGTGCTGGGATGGCTGTGCGGAGCTGT
 ATCACCTGGGTCTGTCCCCCTGGCTCTGTATCAGGCACCTTTATTAAGCTGGGCCCTCAGTGG
 GTGTGGTTTGTCTCCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTCAGGAGGAGGCTGTGA
 GGCTGGAGGGCAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGTATGGGTGG
 GGGCGGTGACTGCCACAGACTTGGTTTTGTAATGATTGTACAGGAATAAACACACCTACGC
 TCCGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 34

MSSNKEQRSVAVFVILFALITILILYSSNSANEVVFHYGSLRGRSRRFPVNLKKWSITDGYVPIL
GNKTLPSRCHQCIVSSSSHLLGTLGPEIERAECTIRMNDAPTGTYSADVGNKTTYRVVAH
SSVFRVLRRPQEFVNRTPETVFIWGPFSKMQKPQGS�RVVIQRAGLVFPNMEAYAVSPGRM
RQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHVHVYGMVPPNYCSQRPLQRMPYH
YYEPKGPDECVTYIQNEHSRKGNNHHRFITEKRVFSSWAQLYGITFSHPSWT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

TTTTCTCATAGTTCGGGCTGTTTGAAGGAAAACATAAATAGGAACATCAGCGCCGCGGGATCGAGCAGAGCTTG
 GAGGAGAACTTCCTACGCTGTTCCGACGAGAGGGGCGAGCTGAAGCCAGTGGCCGAGGTCGTCTGAGCGGCTTG
 GGCAAAAGCTGAAGAGTTCCTTCAGAACAGCTTCTCGGAACAGTACGCCATGAAGTCTCTGTGCATATTTATACGCT
 CTAGGGTAGAGGCTGAAACTAGAAAGTAAGTGGAGTGTCCAGGAGCGGAGCATCTCTTTTGTGTGACCTTGGC
 GGCCATTTGGGAGCTTGGCTTCAGACCTTTTGTATACACATCTGCTGGGACAGATGACGGCGTGGGAGAGGAATG
 AGGCTCTAGGTCACACTGGCTTGCTCTCTAGCCAGCAGGCTGTGTTCTGACTTGAACGAGTCCCTGAC
 GTCACGCTCGAGCTTGGCTCCACGCTCGGAAGCGCCGAGGACATCGTATGCTTGGGCTGCTGGTGGAACTCCCA
 AGATGAATGTAACTCTGAGTGAAGTGAATGAGGAGCTGAATGGTGGATGATGCTGGGTGTCTCTCTATCCACT
 GGCGCTGTGGCGAGGCTGGCCAGCTCTTACACACCACTCTGGGACGAGTACAGTGTGTGGCCGGATGCGCTGGG
 TTTAAGTGGTATGAGGAAAACACAGCACTATTGTCTGCACCTTGAACAGAGTCAAGTATAGATGTGCAGCACT
 TCAGCGCTCAAAACAGAGTGGCTGGAGGCTCCAGAGTAACTACTTACTTACCTCTCCCTTGGGAACTCCAGATT
 TGAATTGCCGCGAGGAGGACGAGGCAATGTACAGTGTGCAGCTTACAAACCAGTACCAGCAAGTGAATGAAC
 CCGCGCTCCGACGACAGGACTCGTGTCCGCCCTCCACCCTGAGGCTCCGCCATATCTACCCCCGAGAGGCC
 CAACACCATCTGTCAACAAAGGCGAGATCTTATTCTGGAAGTGTGTGGCAGTGAATCAACCCGCCAGGCTG
 AACTGGGCAAGGATGGGTCTCAAGTTCACGGCTACACAGACAGCGCTTCTCGTGAAGCACTCTCTATCTGAC
 ACCACGAGGAGGAGGATCAGGCACCTACCGCTGACTGCGCAAGCAATGGGTTGGGACGCGCGGGGCGCGCTG
 ATCTCTACAATCTCAGAGTGTGTAACCCCTGAGGTACCCATGAGCATCTCCAGCTGTGCTATCTCCCTTGGGCG
 CAGAGTGGAGAGCTACCTGTGAGGTCGTGGGAAACCCCCCGCTCGTGCTGGGCTGAGGAATGCTGTGGCC
 TCTTACAGTGCATGGCCAGTCCGAGGCTGGGCTCGGCGCTCGAGTCTCAGCATGGGCTCTGAGGACAGGAGG
 ATAAACCCAGGCTCTGGAGCAATGCTGAGCTGGCTCTGCGCACTCTGCGACACCTCTGTGGTGGGCGGAG
 CTTGAGCAGATGCTGAGGGGGCAACCCGCGCTCCCGAACCCCAACCTCATGTGGGCGCTGCTTCCSCBAAGTGT
 CCAGGAGAAAGGGGACGGGGCTCCGCGGAGGCTCCCATCTCTCACTCCGCGCCAGCATCTCAAGACAGAC
 TCATATGAATGTGTGTGGCGGCTCGGCATGAGGAGCTGGCCGGGCGCCAACTCTCTACTATGTGGTGAACAC
 CGAACAGAGCTCAAAATTTCTCTGACAGTGTGACCATCTTGCATCTTGACCAACAGCAGCGGCTGACCTC
 ACCAGATCTGACCCGGGAGCTTGTATGAGGTGGAGTGTGCACGTCTACAATCTGTGGGAGAGGGGACAGACGCC
 ATGTGCACTTCTCGAATGGAGCGGGGCGCAAACCCAGATCTATGGCCAGAAAGACAGCATCTCAGAGAGA
 ACCCTTGGAGCGAGCTCCCGAGAGCAGCAGCAGCAGACAGCGCGCCTCTCCCGCCAGAGAGCTCCCGACAGG
 CAGTCTCTCTGTGGAGTATGTCAGAGCTCAGTGTGATGCTGATCTCCGTTGGGAATGTGGGTTTCCCAATC
 TCGCGGCTGTCCGTGGATGACGCGGCTTAGAAGAAAGCACTCTTGAAGTTCTGAGGAGGAGGAGGAGGAGG
 CTGGGGGAGTACGCGAGGACAGCCCTCTCTCGGCCCTCATGCTGTGTTCGGGCTACAGCGTCTCGCTGTACAGAG
 CCGCTGGCAGGCTCTTATATCACTTCAGGTGGGCTCAATGAGACCAACCATCTGCTCAAGTGTAGTATGAC
 CAGCAAGTAATAACACAAACCCCAATCTCATGCTTTTCTTATCTATATGACCCACAGACAGCTGACATGATG
 GACACCAAGAGATATGTGTGAAGGGGCAAGTATGTGCATCTGACCCATCTGACCCAGCTGACGACAGAGACTCTC
 GACTATTAGATGTGAGTCTCAATGAAGGAGGGAGAGCGAGTTGACGAAGCTGATGATCTGTGAGACCAAAAGCT
 CGGAAGTCTCTGTGGCAGCGGCTGTGCTGACTGTGCACGCCCAACTCTGGCCCAACAGCAGCGCCCTCTGTAAAC
 ATAGAGCGCCCGTGGGACATGGGCGATGTGGCTCGCTCCAGCGAGCTGCCATCTTATGTTTCTGGGGTGTG
 ACACAGAGACTGGTTCTTCGCGCTCTGACCTCATTCCTCTCTGTGTTGGAGGCGCTGGTCTAAGCAAAAACAT
 CGAGGCCACAGCGAGCTGGACGCCCTACCTTACCTGCTGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
 AATAGGGGCTCGCCCTTCGCTGCTAGTGGGCTACCGGGCATGAAGCCGCCACAGCCTCTACCGCGGAGCTTCAG
 CAGCAGATGTGACACAGAGCGCTGTGTGGAGCAACCATCTTGGAAATGGATATGACCCCAAAGCTACACAGAT
 ACGAGGGGTTCCCAAGTCTAGCGGACGAGGAGGCTTCTTCTATACACTGTCGCGACGCTCACTACACAGCT
 CTCGAGCCCCATCAGCACTGCTGCCAACGAGAGACAGCTGTGCTGTGGGCACTCAGGGTGGAGGAGGCT
 CGACAGCTCTGCTCTGGAAGCACTGTGGACCTCCATTTCTACAGGGGCCCACTGCTGTTGGGCTTGTG
 CCAGTTGAAGAGGTGGACAGTCTGACTCTGCCAAGTGAGTGGAGGAGCTGTGTCCCGACAGCCCGTAGGG
 GCTCTAGTGAGGACAGGAACCTGGAATGCGAGTCTCTCCCGGGGCCATGGTGCTGTGTTTCTTGTAAACACCACT
 TCTCAATATAGCAGAGCTGTAATCCAGCAAGAATCATATATGTTTTTTTTTGTAAAAAAGAGAGAAAAA
 TATGTTTATATCTTGAGAGACAGGAGCACTTATATAGCATATATATATATATATGCAATGTGAATAAAATGTGA
 CTTAACAGAGCTCCACGGAAGAACCTACAGCTGTGGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
 CGAGGCGAGGCTCGAGGAGGCCACAGATAGCTGGCAAGGAGGAGTCCGACGAGAGCTGCTATCAGCAGCT
 TAGGGAAACAGCAAGAGGGGACGGTATCAGCGTGGAGACACCCACAGATGCTGTGATCCGCTGCTAGCGGA
 TTTTCTTCTAAGATGCCCATGAGACAGACCAAGATGTGTACAGCATATGAGCATGTAAAAAACTTCCAGAT
 CAATATCTCTGGCAACATATCTGTAAAAACAAACATCTGTAACCTTCAAAATATGTTTATGCTCTTCTCTGTAAAA

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FIGURE 36

MLRGMTAWRGMREPTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVILGCVVEPP
 RMNVTWRLNGKELNGSDDALGLVLIHTGLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSGNLQ
 IVNASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEARIIPPEAQTIIIVTKGQSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
 AVILYNVQVFEPPEVTMELSQLVPIWQGSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS
 RRALRVLSMGPEDEGVYQCMAENEVGSAAHVVLRTSRPSITPRLWQDAELATGTPPVSPSK
 LGNPEQMLRGQPALPRPPTSVGPASPKCPGKGGAPAEAPIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFRTRRPKPEIMASKEQQIQRDDPGASPQSSSQPDHGRLSPPEAPDRPTISTASE
 TSVYVTWIPRGNGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRV
 RALNMLGESEPSAPSRPYVVSQSGRVYERPVGPIITFTDAVNETTIMLKWMIIPASNNNT
 PIHGFYIYRPTSDNDSDYKDKMVEGDKYWHSISHLQPETSIDIKMQCFFNEGGESEFSNMV
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVGTMAMVARSSDLPYLIVGVVLGSIVL
 IIVTFIPFCLWRWSKQKHTTDLGFPRSALPPSCPVTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRGCPSSAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLNGYDPPSHQITRGPK
 SSPDEGSFLYTLPPDSTHQLLQPHHDCCQRQECPAAVGGQSGVRRAPDSFVLEAVWDPFFHSG
 PPCCGLGLVPVEEVDSPDSCQVSGGDWCPQHPVGAYVGQEPGMQLSPGPLVRVVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

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FIGURE 37

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTC
 CCAGGCTCCCGCGGCCGACCCCGCGCAAC**ATG**CAGCCACGGGCCGCGAGGGTTCCCGCGC
 GCTCAGCCGGCGGTATCTCGCGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC
 CCGTAACCCGCGCGGAGACCACGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCC
 AGCCTCTTACCACGCCGGGTGTCCCCAGCGCCCTACTACCCAGGCCCTCACTACGCCAGG
 CACCCCAAACCTTGGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG
 TGGACGGCCACAATGACCTGCCCCAGGTCCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCAGGACCAGACTGCCGTGCGCC
 TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCTCCTACTCTGAAGTTCGAGCTT
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAAGCTGGCCTGCCTCATTGGCGTGNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT
 ACCTGACACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTTCACCAAGTTTCAGACAC
 CACATGTACACCAACGTCAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA
 CCGCCTGGGCATGATGATAGATTTGTCCTATGCATCGGACACCTTGATAAGAAGGGTCCTGG
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG
 TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT
 GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTTCATCGGGATTGGTGGAATATGACGGGACT
 GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCTTTCGTGGAACCTGCTGCGGGTCT
 TCAGACAAGTGGAAAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCGTGGAGGCTGAGTTT
 CCATATGGGCAACTGAGCACATCCTGCCACTCCACCTCGTGCCTCAGAATGGACACCAAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGAGGTCCTCAAAATGCTC
 CCCCATACCTTGTTCAGGCCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCCAGTGCGTC
 TGCT**GA**CACAGTCGGTCCCCGAGAGGTCAGTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT
 AGTTCATTACAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

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FIGURE 38

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
<subunit 1 of 1, 487 aa, 1 stop, 2 unknown
<MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRLRRLLLLLLLLLLQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPLTTPGTPTKTLDLRGRAQALMRSPFLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLVLSQAPVIFSHSAAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFPYQQLSTSCH
SHLPVQNGHQATHLEVTKQPTNRVFWRSSNASPYLVPGLVAAATIPTFTQWL
```

Important features of the protein:

Signal peptide:

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
 TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAAGCATG
 AAGCTCTTATCTTTGGTGGCTGTGGTCGGGTGTTTGTGGTGCCCCAGCTGAAGCCAACAA
 GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA
 TTTACAACCAGAATGTATCCAGAAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA
 GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
 CACCACCACCATCAAGGTCATCATTGTCTATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT
 ACATGGCCCTTCCTGATGCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
 GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC
 AAGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCTTAGATGGGCTGG
 TGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCAGGCTGGACAAAGCAGGGGG
 CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCGTGTGGCATTTTTCTCCTT
 CTCCTTAACCTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT
 GATCTCTGTTGTCTTCTTGGGTCTTTGGGTTGAAGGAGGGGGAAGGCAGGCCAGAAGGGA
 ATGGAGACATTCGAGGCGGCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG
 CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCTTGGAAGATAAAGCTGGGTCTTCA
 GGAACTCAGTGTCTGGGAGGAAAGCATGGCCAGCATTAGCATGTGTTCTTCTGCAGTG
 GTTCTTATCACCACCTCCCTCCAGCCCCGGCGCTCAGCCCCAGCCCCAGCTCCAGCCCTG
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCCTGGGTCTTCAGGTTGCACTGGA
 AGCTGGTGTTCGCTGTCCCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT
 CTGCTGCCGTTCCCCACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTG
 CACAGTCACTGAGCCAGACGGTCGGTTGGAACATGAGACTCGAGGTGAGCGTGGATCTGAA
 CACCACAGCCCCGTACTTGGGTTGCCTCTTGTCCCTGAACCTTCGTTGTACCACTGCATGGA
 GAGAAAATTTTGTCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAAATTG
 TTTTATTCTCTCA

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FIGURE 40

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSDIRCKCICPPYRNISGHIYNQNVSKDCNCLHVVEPM
PVPGH DVEAYCLLCECRYEERSTTTIKVIVIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

AGCGSGTCTCGGTTGGGTTCCGCTAAATTTCTGTCCTGAGGCGTGAGACTGAGTTTCATAGGGTCTGGGTCCCCGA
 ACCAGGAGGGTTGAGGAAACACAATCTGCAAGCCCCCGACCCCAAGTGAGGGGGCCCGTGTGGGGTCTCCCT
 TCCCTTTGCAATCCCAACCCCTCGGGGCTTCGCTCTTCTGGGGACCCCTCGCCGGGAGATGGCCCGGTTGATG
 CGGAGCAAGGATCTGCTCTGCTGCTGCTCTACTGGCCGGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT
 TCGCGGGCCAAACTCACTCCATCAAGTCCCTCTGGCCGGGGAGACGCCTGGTCAGGCCCAATCGATCTGCG
 GGCATCTACCAAGGACTGGCATTCGGCGGCAGTAAGAAGGGGAAAAAGCTCGGGCCAGGCCTACCCCTGTGAGAGA
 GATTAAGGATGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGCATGGTGTGTGCGGAG
 AAAAAAGAGCGCTGCCACCGAGATGGCATGTGCTGCCCAAGTACCCGCTGCAATAATGGCATCTGTATCCCAAGT
 ACTGAAGGACATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCAACGGTCAATTAC
 TCAAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCAACACTAAGATGTGCACATATAAAGGGGATGAAGGA
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTGCTGCTTTCTGGACCAAAATCTGCAAA
 CCAAGTGTCCATCAGGGGGGAAGTCTGTACCAAAACACGCAAGAAGGGTTCTCATGGGTGGAATTTTTCCAGCGT
 TGGCACTGTGCGAAGGGCCGTCTTTCGAAAGTATGAAAGATGCCACCTACTCTCCAAAGCCAGACTCCATGTG
 TGTGAGAAAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAG
 CATGGTGGAAAAATAAGGTTGAGATGCAGAAAGATGGCTAAAAATAAGAAACGTGATAAGAATATAGATGATCACAA
 AAAGGGAGAAAGAAAAATGAATGAATAGATAGGTTGACAAATGCAGTGCAGCCAGTGTTCCATTATG
 CAECTTGTCTATGTAATAATGTACACATTTGTGGAAAAATGCTATTATTAAGAGAACAGCACACAGTGGAAATT
 ACTGATGAGTAGCATGTGACTTCCAAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTCCTTCAGATGTCTGATTGC
 TTATACAAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAAACAAAATACTCTAGAATAACTTGTTA
 TACAATAGGTTCTAAAAATAAAATGCTAAACAAGAAATGAAACATGGAGCATGTTAATTTACAACAGAAAAT
 TACCTTTTGATTGTAAACTACTCTGCTGTTCAATCAAGAGTCTTGGTAGATAAGAAAAAATCAGTCAATAT
 TTCCAAATAAATGCAAAATAATGGCCAGTTGTTTAGGAAGGCCCTTTAGGAAGCAAAATAAACAACCAACAGAC
 CCACAAATACTTTTTTTCAAAATTTTAGTTTTACCTGTAATTAATAAGAACTGATAAGAACAAAAACAGTTCC
 TFCAGATCTACGGAATGACAGTATATCTCTTTATCTCTATGTGATTCTGCTCTGAATGCATTATATTTTCCA
 AACTATACCCATAAATGTGACTATGTAATAAATACTTACACAGAGCAGAATTTTCACAGATGGCAAAAAAATTTAA
 GATGTCCAATATATGTGGGAAAGAGCTAACAGAGAGATCATTTATTTCTTAAGAGATTGGCCATAACCTATATTT
 GATAGAATTAGATTGGAATACATGTATTCTACATACTCTGTGGTAATAGCAATTAAGCTGGATTGCTACTG
 CACTGGAGTAAGCAAGAAAAATGGGAAAACTTTTTCGTTTGTTCAGGTTTTGGCAACACATAGATCATATGTCTG
 AGGCACAAGTTGGCTGTTCACTTTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT
 CATATATTTTACTATGCAGATGAATTCAGTGTGAGGTCTGTGTCGCTACTATCTCAAAATTTATTTATTTATAG
 TGCTGAGATCCTCAAAATATCTCAATTTCAGGAGGTTTCACAAATGTACTCTGAGGTAGACAGAGTAGTGAGG
 TTTCAATGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTTCCCAACCTCTGCAGCATCTG
 CTTTATTTGCCAAAGGGCTAGTTTCGGTTTTCTGCAGCCATTGCGGTTAAAAAATAAAGTAGGATAACTTTGTA
 AACTGCATATTGTCTAATCTATAGACACCAACAGTTTCTAAATTTCTTTGAAACCACTTTTACTCTTTTTTAAACT
 AACTCAGTTCTAAATACTTTGTCTGGAGCACAAAACAATAAAGGTTATCTTATAGTCTGACTTTAAACTTTTG
 TAGACCACAATTCACTTTTAGTTTTCTTTTACTTAAATCCCACTCTGCAGTCTCAAAATTAAGTTCTCCAGTAG
 AGATTGAGTTTGAAGCTGTATATCTATTAAAAATTTCAACTTCCACATATATTACTAAGATGATTAAAGACTTA
 CATTTTCTGCACAGGTCTGCAAAAACAAAAATATAAACTAGTCCATC CAAGAACCAAGTTTGTATAAACAGGT
 TGCTATAAGCTTTGAAATGAAATGGAACATTTCATAACAACTTCTATATAACAAATTTATATAATTTACAAAT
 TGGTTTCTGCAATATTTTCTTATGTCCACCCCTTTTAAAAATTTATTTTGAAGTAATTTATTTCAGGAAATG
 TTAATGAGATGATTTTCTTATAGAGATTTTCTTACAGAAAGCTTTGTAGCAGAAATATATTTCAGCTATTGAC
 TTTGTAATTTAGGAAAAATGTATAATAGATAAAATCTATTAATTTTTTCTCTCTTAAAACTGAAAAAATAAA
 AAAAAAAAAAAAAAAAAA

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FIGURE 42

MAALMRSKDSSCCLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
 FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKRCHRDGMCCPSTRCNN
 GICIPVTESILTPHIPALDGTRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCILRS
 SDCIEGFCCARHFWTICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
 SKARLHVCQKI

Signal peptide:

amino acids 1-25

FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGCCCTCCCAAA
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGCCAACATCAGCTTTTAAAAATTGATT
 TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTGAGAATGAGGAAGGA
 TAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG
 TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG
ATGTGTTTTAAAGCCTTGGGCAGAAATTCGTATTGTTGAGGATTGTCTTTTATCCCCCT
 TTTAAAGTCATCCGTCCTTGGCTCAGGATTGAGAGAGCTTGCACCACCAAAAAATGGCAACA
 TCACCAGCTCCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC
 CCAAGTACACAGCAGAATAGTACAAGTCACCCTACAACACTACTTCTTGGGACCTCAAGCC
 CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC
 CAGTTCCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCAGTGTTCCTCCT
 CCTGGTTTGGAGTCCTTTCCCTCCAGGCAAAACTTCGAGAATCAACACCTGGAGACAGTCC
 CTCCACTGTGAACAAGCTTTTGCAGCTTCCAGCAGACCAATTGAAAAATATCTCTGTGTCTG
 TCCACCAGCCACAGCCCAAACACATCAAACCTTGCTAAGCGGCGGATACCCCCAGCTTCTAAG
 ATCCAGCTTCTGCAGTGGAATGCCTGGTTCAGCAGATGTCACAGGATTAATGTGCAGTT
 TGGGGCTCTGGAATTTGGGTCAGAACCTTCTCTCTGAAATTTGGATCAGCTCCAAGCAGTG
 AAAATAGTAATCAGATTTCCATCAGCTTGATTGCAAGCTTTAAGTGAGCCTTTGAATACA
 TCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTTCCGTCATTACCTCCTG
 CAGTCTGACAAGCTCATCACTGAATTCGTAGTCCAGTAGCAATGTCTTCTCTTTATGACC
 AGAGTTCTGTGCATAACAGGATCCCATAACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA
 GGAACCATCATGAATGGACATGGTGGTGGTCTGAAGTCAGCAGACACTAGACAGTAAGTATAG
 CAGCAAGCTACTCTTGTGATGGCTGGTGCCAACCAAACAGAGGAAGAGGATAGCTCACGTGA
 TGTGGAAAAACACAGTTGGTCAATGGCTCATTCTGTTAAAGCAGCCCTTTTGCTTTTTTGT
 TTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT
 GGTGGTCTCATATTTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCAT
 TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCCATAATCCCAGTGCTTTGGGGGGCC
 AAGGCAGGCAGATTGCCAAGCTCAGGAGTTTGAGACCACCCTGGGCAACATGGTGAAACTC
 TGTCCTACTAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGGTGCCTGTAATCCCAG
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC
 GTCTGAAAAGA

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FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTTSSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPP
PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPKHKIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTTSSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP
GTIMNGHGGGRSQQTLDISKYSSKLLLSWLVPKQKRIAHVMWKTVPVGQWLIR

Signal peptide:

amino acids 1-24

FIGURE 45

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCCATGCGCTGCCATCCCCGAATCCTGCT
 TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCCGCCTGGAGGTACCGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGCGGCACCCGCGCTTCTGACCTGCGTGAAACCGGGGACGTGT
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGACTGGGACCGGCAGCCGCCGGG
 GTCCCGCAGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCTA
 CGGGCCCCCTTTTCTGCGGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCGAGGGCACCTACTCCTGCCACCTGCAC
 CACCATTACTGTGGCCTGCACGAACGCCGCGCTTCCACCTGACGGTGCGCGAACCCACGC
 GGAGCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCAGGCCCAG
 ACCCCACACTGGCGCGCGGCCACAACGTCATCAATGTATCGTCCCCGAGAGCCGAGCCCAC
 TTCCTTCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTATCCTGCTACTGGTCAC
 TGTCTCCTGGCCGCCGCGAGGCGCGGAGGCTACGAATACTCGGACCAGAAGTCGGGAA
 AGTCAAAGGGAAAGGATGTTAACTTGGCGAGTTCGCTGTGGCTGCAGGGGACCAGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCGGAAGGAGAACT
 GCAAATAGGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC
 CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTCCAGCGGCTGGTCCCGCTTTCCT
 GGAATTTGGCCTGGGCGTATGCAGAGGCGCCCTCCACACCCCTCCCCAGGGGCTTGGTGGC
 AGCATAGCCCCACCCCTGCGGCCTTTGCTACAGGGTGGCCCTGCCACCCCTGGCACAACC
 AAAATCCCCTGATGCCCATCATGCCCTCAGACCTTCTGGGCTCTGCCCGCTGGGGGCGCTG
 AAGACATTCCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAATGGGGTCAGCCTCA
 GGGCAGGAGTCCCCTCCTCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTTGAGGA
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT
 CCTCCTGGGGTGTGCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG
 GCACCATCTGTTCTCCCGAGGACCTGCTGACTTGAATGCCAGCCCTTGTCTCTGTGTTG
 CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTTCTCTGCCCATCCCTACCCTAGCCTTG
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCTGACACCCCTCCCTT
 GGACTCTGCCTGGGCTGGAGCTAGGGCTGGGGCTACATTGGCTTCTGTACTGGCTGAGGA
 CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTGCCACTCTCAGACCCACATTT
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTAAAAA
 AAAAA

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FIGURE 46

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618

<subunit 1 of 1, 341 aa, 1 stop

<MW: 38070, pI: 6.88, NX(S/T): 1

MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTDHRVVEEAQQVVHWDQPPGVPHDRADRLDL
YASGERRAYGPLFLDRVAVGADAFERGDFSLRIEPLVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEPPPRGSPNGSSSHSGAPGPDPTLARGHNVINVIVESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSQKSGKSGKGDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDLDKGFRKENCK

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGGCGGCGTGGCGCAGCGGCAGC**ATG**GCCGTGTGCTCAGAGGACGACTTT
 CAGCACAGTTCAAACCTCCACCTACGGAACACACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC
 ACTGCTTGAGAAGCTGCTGGACCGCCCGCCCCCTGGCCTGCAGAGGCCCGAGGACCCTTCT
 GTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCAGTCTACTGCCATGGAACCTCTTTT
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCTCTCCAGCCCAGCCACCAGGGGA
 GGACCTTGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCTCCACCG
 TGCCCTCCATGCTGTGCCTGGTGGCCAACTTCCTGCTTGTCAACAGGGTTGCAGTCCACATC
 CGTGTCTTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAA
 GGTGGACACTTCTCCTGGACCCGTGGTTTTTTTGGGTCACCAATTGGTCTGGATGGTGATCC
 TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTTCTATCC
 AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC
 ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG
 CCACCATCTTCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC
 AGGTACTACATGAGGCCTGTTCTTGCGCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCA
 GGACTCCCTCAGTGCCCTTTCGGTGGCCTCCAGATTCAATTGATTCACACACACCCCTCTCC
 GCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTCACTACGTCTTCTTCATCAC
 AGCCTCATCTACCCCGCGCTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT
 GTGGACCACCAAGTTTTTCATCCCCCTCACACCTTCTCTGTACAACCTTTGCTGACCTAT
 GTGGCCGGCAGCTCACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCCTCCACAGG
 TTCGTGCTCCTCCGGACCTGCCTCATCCCCCTCTTCGTGCTCTGTAACACCAGCCCGCGT
 CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGCTCCCTGTCTGG
 GGCTCAGCAACGGCTACCTCAGCACCTTGGCCCTCCTCTACGGGCCCTAAGATTGTGCCCAAG
 GAGCTGGCTGAGGCCAGGGAGTGGTGATGTCTCTTTATGTGTGCTTGGGCTTAACACTGGG
 CTCAGCCTGCTTACCCTCCTGGTGCACCTCATCT**TAGA**AGGGAGGACACAAGGACATTGGTG
 CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAAGGCC
 TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCA
 GTGAGCCACGTCATGCCCATTCCTGTCAAGGCAGATATTCAGTCTATTAACAGAACACT
 CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTACAGCTGATGGTTA
 ACATTCACCTTTCTTTAGCCCTTCAAAGATGCTGCCAGTGTTGCGCCTAGAGTTATTACA
 AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCCAGCTGCGCTCATTCAGCT
 GACAGCAGATGCAAGCAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAAATGGA
 AGTCCCTGGCATGGTCAGTCTCCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT
 CGGGGTGAACAACCTGCCCACTAACCAGACTGGAAAACCCAGAAGATGGGCTTCCATGAAT
 GCTTCATTCAGAGGGACAGAGGGCTCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG
 TTTTCAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTC
 TTTCAGTGTTCTGTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC
 GTATTCAAAAA

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FIGURE 48

MAVVS EDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGQLQRPEDRFCGTYYIFFSLGI
 GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL
 LVNRVAVHIRVLASLTVILAIFMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
 YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRSALAFFLTATIFLVLCMGLY
 LLLSRLEYARYYMRPVLAHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRPILKKTASLGF
 CVTYVFFITSLIYPVCTNIESLNKGSGLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP
 GPNSKALPGFVLLRTCLIPFLVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL
 LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
 305-330, 448-472

FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCTGCTGTACCAAGAGCTGGAGACACCA
TCTCCACCCGAGAGTCAATGGCCCCATTGGCCCTGCACCTCCTCGTCTCGTCCCCATCCTCC
TCAGCCTGGTGGCCTCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGC
ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCT
GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGC
TCAGCGATGCTGGACACAAGGTCACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC
TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCAG
CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCTGGGGCTCAACCTGACCAAGTTCACCC
AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG
AAGGTGCCCCGAGAAGCTGGGCTACGCCTTGCGTCCCCAGGAAAAGGGCCACTCGCCCCAAGA
CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG
CGATGAAGAAGTTTGAAGGCACACGCTCTTGGAATATCTTCGCGGGAGGGGAACCTGAGC
CGGCCGGCCGTGCAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT
CGCCGAGGCCCTCCGGGCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG
GTGGCTGGGACCTGCTGCCGCGCGCGTGTGAGCTCGTGTCCGGGCTTGTGCTGTTGAAC
GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC
CCCGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGACCGG
CGGTGAAGCGCATACCTTCTCGCCGCCGTGCCCCGCCACATGCAGGAGGCGCTGCGGAGG
CTGCACTACGTGCCGGCCACCAAGGTGTTCTTAAGCTTCCGCAAGGCCCTTCTGGCGCGAGGA
GCACATTGAAGCGGCCACTCAAACACCGATCGCCCGTCGCGCATGATTTTCTACCCGCCGC
CGCGCGAGGGCGCGCTGCTGCTGGCCTCGTACACGTGGTCGGACGCGGCGGCAGCGTTTCGCC
GGCTTGAGCCGGGAAGAGGCGTTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC
TGTCTGCGCCAGCTCTGGGACGGCACCGCGCTCGTCAAGCGTTGGGCGGAGGACACGACA
GCCAGGGTGGCTTTGTGGTACAGCCGCCGCGCTCTGGCAAACCGAAAGGATGACTGGACG
GTCCCTTATGGCCGCATCTACTTTGCCGGCGAGCACACCGCTACCCGCACGGCTGGGTGGA
GACGGCGGTCAAGTCGGCGCTGCGCGCGCCATCAAGATCAACAGCCGGAAGGGGCTGCAT
CGGACACGGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGGCAGGGGCATGTGCATGGG
GTGGCCAGCAGCCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCTCCAGTCCAAGG
CCAGTTATCTCTCCAAACACGACCACACGAGGACCTCGCATTAAAGTATTTTCGGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 50

MAPLALHLLVLVPIILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVWGLNRTLKPQRV
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGVALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSEDGEFFYLSFAEALR
AHSCLSDRLQYSRIVGGWDLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL
KVLKADVLLTASGPAVKRITFSPLPRHMQEALRRLHYVPATKVFLSFRFPFWREEHIEGG
HSNTDRPSRMIFYPPREGALLASYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVAASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRTSH

Signal peptide:

amino acids 1-21

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FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTGCCTGCAT
 GGACCGCTCTGAAGCCACCCCTGTCTCTGGAGGAACACAGAGCAGGGAAGAAGGACAGGGACTCGTGTGGCAGGAA
 GAACCTCAGAGCCGGGAAGCCCCCATTCCTACTAGAAGCACTGAGAGATGCGGCCCCCTCGAGGGGTCTGAATTTCTCT
 GCTGCTGTTTCAACAAGATGCTTTTATCTTTAACTTTTGTCTTCCCACTCTCCGACCCCGCGGTGTATCTGCAT
 CTTGACATTTGGAGCTGCCATCTTTCTGTGGCTGATCACCAGACCTCAACCCGCTTTACCTCTTCTTTGACCTGAA
 CAATCAGTCTGTGGGAATTGAGGGAGGAGCAGGGAAGGGGTTTCCCAAGAAGAACATGACCTAAACAAGTTGCTG
 CTTCTCAGATGCCAAGACTATGTATGAGGTTTCCAAAGAGGACTGCGCTGTCTGACAAATGGGCCCTGTCTTGGG
 ATATAGAAAACCAAACAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGATACCTGGGTTC
 CTGCTCTCTTGCAATAAGGTTATAAATCATCACCAGACCAAGTTTGTCCGCATCTTTGCTCAGAATAGGCCAGAGTG
 GATCATCTCCGAATTTGGCTTGTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTTGGGACCAGAGC
 CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAGGCATTTGGTGTGAT
 AGGGAATGTAGAGAAAGGCTTCAACCCGAGCCTGAAGGTGATCATCCTTATGACACCCCTTTGATGATGACCTGAA
 GCAAAGAGGGGAGAGAGTGGAAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAGAGCACTTCAG
 AAAACCTGTGCCTCCTAGCCAGAAGACCTGAGCGTCATCTGCTTACCAGTGGGACCACAGGTGACCCCAAAGG
 AGCCATGATAACCCATCAAAATATTGTTTCAAATGCTGCTGCCTTCTCAAATGTGTGGAGCATGCTTATGAGCC
 CACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAAGAGGATGTACAGGCTGTTTGTGTA
 CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTCGGTTGCTGGCTGACGACATGAAGACTTTGAAGCC
 CACATTTGTTTCCCGCGGTGCTCGACTCCTTAACGAGATCTACGATAAGGTACAAAAATGAGGCCAAGACACCCCT
 GAAGAAGTTCTTGTGAAGCTGGCTGTTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG
 TTTCTGGGACAAGCTCATCTTTCAAAGATCCAGGACAGCCTGGGCGGAAGGGTCTCGTGTAATTTGCACTGGAGC
 TGCCCCCATGTCCACTTCACTGATGACATTTCTTCCGGGCAGCAATGGGATTCAGGTGTATGAAGCTTATGGTCA
 AACCAAGTGCACAGGTGGCTGTACATTTACATTACCTGGGGAAGTGGACATCAGGTCAAGTTGGGGTGGCCCTGGC
 TTGCAATTTACGTGAAGCTGGAAGATGTGGCTGACATGAACCTTTACAGTGAATGAATGAAGGAGAGGTCGTGAT
 CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCTGAGAAGACACAGGAAGCCCTGGACAGTGATGGCTG
 GCTTACACAGGAGACATTTGGTCCGTCCCGAATGGAAGCTCTGAAGATCATCGACGTAAGGAGCATTTT
 CAAGCTGGCCCAAGGAGAATACATTGCACCAGAGAAGATAGAAAATATCTACACAGGAGTCAACCAAGTGTATACA
 AATTTTTTGTACACGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGGTCTCTGACACAGATGTACTTCCCTC
 ATTTGCAGCCAAAGCTTGGGTTGAAGGGCTCCTTTGAGGAACCTGTGCCAAACCAAGTTGTAAAGGAGAGCCATT
 AGAAGACTTGCAGAAAATTTGGGAAGAAAGTGGCCTTAAACCTTTTGAAACAGCTCAAAGGCATTTTCTCATCC
 AGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTGAAAGCAAGCGAGGAGAGCTTTCCAAATACCT
 TCGGACCCAAATTGACAGCTGTATGAGCACATCCAGGATAGGATGAAGTACTTAAATGACTCCCGGCCACTG
 TGCACTGCTTGTGAGAAAATGGAATAAAAACTATTCTTACATTTGTTTGGCTTTCCCTCCTATTTTAAAAAC
 TGTTAAACTCTAAAGCCATAGCTTTTGTATTTATATTGAGACATATAATGTGTAACCTTAGTTCCCAATAAATCA
 ATCCTGTCTTTCCCATCTCTCGATGTGTGCTAATATTAAAGGCTTCAGGGCTACTTTTATCAACATGCCTGTCTTCAA
 GATCCAGCTTATGTTCTGTGTCTCTTATGATTTTCAAACCTTAATACTATTAGTAACACAGATCTTCAAAGGT
 CAAAGGGACCCCTCTGTGCCCTTCTCTTTGTTTGTGATAAACATAACTTCCCAACAGCTCTATGCTTTATTATCA
 TCTTCTACTGTTCACAACTAAGAGTTTAAATTTCTGAAAACCTGCTTACCAATCATGTTTCTTAGCCATCCAC
 AAACCACTAAATTTTAGTTTGTAGCCTATCACTCATGTCAATCATATCTATGAGACAATGTCTCCGATGCTCTA
 TCTGCTGATTTAAATTTGTGATCTGAAGGGAAGTTTGAATCATACCAACATTTCTTAACTCTCTAGTTAGATA
 TCTGACTTGGGAGTATTAATAATTTGGGCTATGACATACGTGCAAAAGGAATGCTGTTTAAAGCATTTATTA
 CAGTAGGAACTGGGAGTAAATCTGCTTCCCTACAGTTTGTCTGAGCTGGAAGTCTGCGGGGAAGGATTGACA
 GGTGGGCCCAGTGAACTTTTCAGTAAATGAAGCAAGCACTGAATAAAACCTTCTGAACCTGACCAAAAGATCT
 ACAGGCAGCAAGATGCCACACAAGGCTTATTTCTGTGAAGGAACCACTGATCTCCCAAGCTTGGATT
 AGAGTTCTCTGCTTACTTACCACAGATAACACATGTTGTTTCTACTTGTAAATGTAAAGTCTTTAAATAAAC
 TATTACAGATAAAAAA

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FIGURE 52

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775
<subunit 1 of 1, 739 aa, 1 stop
<MW: 82263, pI: 7.55, NX(S/T): 3
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CCFSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLKVIIIMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIIVSNAAFLKCEVHAYEPTPDDVAISYLPPLAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMTLKTLPFAVPRLLNRIYDKVQNEAKTFLKKFLLKLA
VSSKFELQKGIIRHDSFWDKLIFAKIQDSLGGVRVIVTGAAPMSTSVMTFFRAAMGCQVY
EAYQTECTGGCTFTPLGDWTSGHVGVPLACNYVKLEDVADMNFTVNNEGEVCIKGTNVFK
GYLKDPEKTQEALDSGDWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR
SQPVLQIFVHGESLRSSLVGVVVPDPTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPFESIENGLLTPTLKAKRGELSKYFRTQIDSLYEHIQD
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Important features:

Type II transmembrane domain:

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGCGGAGGCCGCGCGAGCCGGGCCGAGCAGTGAGGGCCCTAGCGGGGCCGAGCGGGG
 CCGGGGGCCCTAAGCCATTCTGAAATCATGGGCTGGCCAGGACATTGGTGACCCGCCAAT
 CCGGTATGAGCAGCTGGAAGCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG
 AGCTGTGTACCTTACCTGGAAGTATAAATGACAAACCAGCGGGCCCTGCGGAGATTTCTGTCA
 GACAGGGGCGGTGCTTTTCTCTGCTGGTGACTGTCAATTGTCAATATCAAGTTGATCCTGGACA
 CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGACGAAGACTATGATGAGGCC
 CTAGGCCGCTGGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTGGACGTAGA
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACACGGTGCTGGAGGATG
 AGGCCCGGGAGCAGGGCCGGGCGATCCATGTCATTGTCTCAACCAGGCCACGGGCCACGTG
 ATGGCAAACGTTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCTCT
 CAACATGGTAGCGCCCGGAGTGCTCATGTCACTGTCAAGGATGAGGGCTCTCTCCACC
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCGAGCCAGGCTGGCCCTGGGG
 TGGAGGGACACATGGGCTCTGCTGGGACGAAAAGGAGGCTCTGTCTTCGGGGAGAAACATTCT
 TAAGTACCTGCCCTCTCTTCTGGGGGACCCAGTCTGCTGAAGACAGATGTGCCATTGA
 GCTCAGCAGAAGAGGCGAGAGTGCCATCTGGGCGAGACAGAGCTGAACCGTCGCCGCCGGCGC
 TTTCTGCGAAGGTTGAGGGTATGGAAGTGTATGCAGTGAAGGACCCACACCCATCGA
 GTTCAGCCCTGACCCACTCCCAGACAAAGGTCCTCAATGTGCCCTGTGGCTGTCAATTGAG
 GGAACCGACCAATTACCTGTACAGGATGCTGCGCTCTCTGCTTTACGGCCAGGGGGTGCTCT
 CCTCAGATGATAACAGTTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGCACT
 GTTTGGTCTGAGGGGCTCCAGCATACTCCCATCAGCATCAAGATGCCCGCGTGTCTCAGC
 ACTCAAGGCTGACGCTCTGCTGACCTTTCAACCTGTTCCGGAGGCCAAGTTTGTCTGTGGTT
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTTCAGTTTCCGAGCCAAATCCATCCACCT
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCTTGAATGACCAAGGGGTATGAACACA
 CGGCTGAGGACCCAGCATACTGTACCGGTGTGGAGACCATGCTGGGCTGGGCTGGGTGCTC
 AGGAGGTCCTTGTACAAGGAGGAGCTTGAGCCCAAGTGGCTACACCGGAAAAGCTCTGGGA
 TTGGACATGTGGATGCGGATGCCTGAACAACGCCGGGGCCGAGAGTGATCATCCCTGACG
 TTTCCCGATCTTACCCTTTGGCATGCTCGGCCCAACATGAATGGCTACTTTTACAGAGGCC
 TACTTCAAGAAGCACAGATTCAACACGGTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCT
 GAAGAAAGAAGCTTATGAAGTGAAGTTTACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC
 ACAGCAAGAACCCTTGTGAAGACTCTTCTGCGACACACAGAGGGCCACACCTACGTGGCC
 TTTATTTCGAATGGAGAAAGATGATGACTTACCACCTGGACCCAGCTTGCCAAAGTGCCTCA
 TATCTGGGACCTGGATGTGCTGGGCAACCATCGGGGCTGTGGAGATTTGTTCCGAAGAAGA
 ACCACTTCTGTGTGGTGGGGGTCCCGGCTTCCCCCTACTCAGTGAAGAAGCCACCCCTCAGT
 ACCCAATTTTCTGGAGCCACCCCAAGGAGGAGGAGCCGAGAGCCGAGACAGAC
 ATGAGACCTCTCCAGGACCTGCGGGGCTGGGTACTGTGTACCCCCAGGCTGGCTAGCCCT
 TCCCTCCATCTGTAGGATTTTGTAGATGCTGGTAGGGGCTGGGGCTACCTTGTTTTAACTA
 TGAGACTTAATTAACCTCAAGGGGAGGTTTCCCTGCTCCAACACCCCGTTCTGTGAGTT
 AAAAGTCTATTTATTTACTTCTCTTGTGGAGAAGGGCAGGAGACTGCGGAATCATTAAG
 ATCCCTAGCAGCTCATCTGCCCTTGAATACCTCACTTTCCAGGCTGGCTCAGAACTCA
 ACCTATTTATTGACTGTCTGAGGGCTTGAAACAGGCCGAACCTGGAGGGCTGGATTCT
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAACCTGCTGTGCC
 CAACCCATGGACAGGCCAGCTGGGGCCACATGCTGACACAGACTCACTCAGAGACCCCTTA
 GACACTGGACAGGCTCTCTCAGCCTTCTCTTTGTCCAGATTTCCAAAGCTGGATAAGTT
 GTTCATTGATTAAAAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 54

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
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REQGRGIHVIVLNQATGHVMAKRVDFTYSPHEDEAMVLFNLMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTWAFVGRKG GPVFGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRRRRRFC SKVEGYGSVCCKDPTPIEFSPDPLPNKVLNVPVAVIAGN
RPNYLYRMLRSLLSAQGVSPQMITVFDIGYEEPMDDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPFAKFAVVEEDLDIAVDFFSFLSQSIHLLEEDDSLVCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRRLSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFTVPGVQLRNVDLSLKEAYEVEVHRLLSAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLVDVRGNHRLWRLFRKKNH
FLVVGVPASPYSVKKPPSVTPIFLEPPPKKEEGAPGAPEQT
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Important features of the protein:

Transmembrane domain:

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

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FIGURE 55

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAAC TGGAAAGCCCACTCTCTTGGAAACCACCACAC
 CTGTTTAAAGAACCTAAGCACCATTAAAGCCACTGGAATTTGTTGCTAGTGGTTGTGGGTGAATA
 AAGGAGGCCAGAATGCGATGATTTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTA
 CGTGGCCGGAAATCATTCCTTGGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTTTGG
 GTGCTGGCCTTCTCTGTGGAATCTGCTTGGCAGTCATCGTGCCTGAAGGATGACATGCCCTTTATGAA
 GATATTTCTGAGGGAAACACCAAGCAAGTGAACACATAATGTGATTGCATCAGACAAAGCAGC
 AGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCACACACAGCTGCATGCCTATATTGGTG
 TTTCCCTCGTTCTGGGCTTCGTTTTCATGTTGCTGGTGGACAGATTGGTAACCTCCATGTGCATTCT
 ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCAAAAATCACCACCACGCTGGGTCTGGTTGTFCCA
 TGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCAGGTTAATTG
 TGTTTGTGGCAATCATGCTCATAAAGCACCAGCTGCTTTTGGACTGGTTTCCCTCTCTTGATGCATGCT
 GGCCTTAGAGCGGAATCGAATCAGAAAGCACTTGTCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCAT
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAGAAGCCCTTTCAGAGGTGAACGCCACGGGAGTGG
 CCATGCTTTTCTCTGCCGGGACATTTCTTTATGTTGCCACAGTACATGTCTCCCTGAGGTGGGCGGA
 ATAGGGCACAGCCAAAGCCCGATGCCACGGGAGGGAGGCCCTCAGCCGCTGGAAGTGGCAGCCCT
 GGTTCCTGGGTTGCCCTCATCCCTCTCATCTGTCACTAGGACACCAGCATTAATGTTCAAGTCCAGC
 TGTGTCAGGCGCGTTTGGCTCAGTGAGAACAGCCGCGCAGTGCAGCTACTCACTTCTCTCAGTC
 TCTTGCTCACTTGGCAGTCTCTACATGTATTCTAGAGTCCAGAGGGGAGGTGAGGTTAAACCCCTG
 AGTAATGGAAAAGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTATAGACATCCCATTTGTGT
 TATCTTTTAAAGGCCCTTGACATTTTGGCTTTTAATATTCTCTTAAACCCATTTCTCAGGGAAGATG
 GAATTTAGTTTTAAGGAAAAGAGGAGAACTCATACTCACAATGAAATAGTGATTATGAAAATACAGT
 GTTCCTGTAATTAAAGCTATGTCTCTTTCTTCTTAGTTAGAGGCTCTGCTACTTATCCATTGTTTTT
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 GCACCCATCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGCTCAGGAAAATGATAGC
 AAGACACATTGAAAGCTCTCTTTATACTCAAAGAGATATCCATTGAAAAGGGATGCTAGAGGGATT
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 TGGGAGGAGCTTCAAAGAGGTGACTGGTATTTGTAGCATTCCTTGCAGAGTTCCTTTGCGAAT
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 CAGTCAGATCAAAAGTGCTTTGGAAATTAAGGGATATTAATATTTAAGTGATTTTGGATGGTTAT
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 TTTTTTTTTAATTATTCTCTTAGCAGATCAGCAATCCCTCAGGGACCTAAATACCTAGGTCAGCTTT
 GGCAGCACTGTGCTTCTCACAATACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGTTGGCTTA
 TTGATTTAAAGCTATTGGAATCATGTCTTGTCTTCTGCTTTCTTTGCTTTCTTTCTTCTTAACTTT
 TCCTCTAGGCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTTAATATTGTGTGGGATGAATT
 CTTATCAGGACAACCACTTCTCGAAGTGAATAATGAAGATAATAATATCTTTATTTCTTTATCCCCCT
 CAAAGAAATTACCTTTGTGTCAAATGCCGCTTTGTTGAGCCCTTAAATATACCACCTCTCATGTGTAA
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 ATTTTTTTTTTCATTTTGGCAAAATTTTGTAAACCTGTCTTGTCAAATAGTGTAATATTGTAT
 TATTAATTTTATTTTACTTTCTATACCATTTCAAACACATTACACTTAAAGGGGAACCAAGACTAGTT
 TCTTCAGGGCAGTGGACGTAGTAGTTTGTAAACAGTTTCTATGAGCATAAGCTAGCATGCTCATG
 ATTTATTTCTCTCATGAATTTGTCAGTGGATCAGCAGCTGTGGAATAAAGCTTGTGAGCCCTGTCT
 GGCCACAGTAGGAAAGTAGCACAATAAGGATACAGTTGATGTAGCTTTGGCAACAATTTGCATACA
 ATTTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAAATGACTTCCTTGATTGGATGTTAACAGCT
 GACTGGTGTGAGCACTTAGGTTTCATCTAGTCCTTCAAACCTATATGGTTGCCTAGATTCTCTCGGA
 AACTGACTTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAAA

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

FIGURE 57

GCTCGAGGCCGGCGGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCGGATCCC
CGAGTGGCGGGCGGAGCCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG
GAAACGGGCGTCGAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC
ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGAT
CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA
AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC
CACAACTTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTGGTGAA
TAACATCACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGA
GGAATTACGGCAGGCTGCAGCAGGATGTCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG
AGGAAGTTCTCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
TGAGGAGCGAATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA
GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
GCAGCAGGCTGCCACACACAGAGGTGCCACAAGGGAAGGGAACGTGCTTGTTAACAGCAA
GTCCCAGACACCAGCCCCAGTTCGGAAGTGGTTTTGGATTCAAAGAGACAAGTTGAGAAA
AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG
CCAGGCCGGGAGCAGGTGGTGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG
AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCTAGTGAGCCAGGAAAATCCAGAGA
TGGAGGGCCCTGAGCGAGACCAGCTTGTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT
GCCGGGGAAGGGAGAAACCAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA
TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG
TTTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG
AATCATACACTCTGAATTGAACTGGAATCATATTTTCAACAGGGCCGAAGAGATGACTA
TAAATGTTTCATGAGGACTGAATACTGAAAACGTGAAATGTACTAAATAAATGTACATCTGA

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FIGURE 58

MMGLGNRRSMKSPPLVLAALVACIIVLGFNYWIIASSRSVDLQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSNNNDQRQQQLQALSEPQPRLQAAGLPHTTEVPQGKGNVLGNSKSQTPAPSSSEVVLDSCR
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

FIGURE 59

GGATG CAGAAAGCCTCAGTGTGGCTCTCTGGCCTGGGTCTGCTTCTCTTACGCTGGCATTGCCCTCTTCA
 CCAGTGGCTTCTCTGCTCACCCTTTGGAGCTCACCAACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC
 TGGCATGGGGAGGCCAAGGGAACCTGGGGCTGCTGGATGGCTTCCCGATTTTCGGGGTTGTGTTGGTGCTGA
 TAGATGCTCTGCGATTTGACTTCGCCAGCCCCAGCATTACACGCTGCCTAGAGAGCCTCTGCTCTCCCTACCTC
 TCTCGGGCAAATCAGCTCCTTGACAGAGGATCTGGAGATTACGCCCAACCATGCCGGCTTACCCGATCTCAGG
 TTAGCCCTCTTACCAACACCATTCAGCGCCTCAAGGCCCTCACCCTGGCTCAGCTGCCTACCTTTATTGATGCTG
 GTAGTAATCTCGCCAGCCAGCCATAGTGGGAAGACAATCTCATTAGCAGCTCACCAGTGACGGAAGGCGGTAG
 TCTTCATGGGAGATGATACCTGGAAAGACCTTTTCCTGGTGCTTTCTCCAAAGCTTTCTCTTCCCATCCTTCA
 ATGTCAGAGACCTAGACACAGTGGACAATGGCATCTCGGAACACCTCTACCCCAACATGGACAGTGGTGAATGGG
 ACGTGCTGATTGCTCACTTCCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCTGAAATGGGCA
 AGAACTTAGCCAGATGGACAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATTGACACACTGCTGGTAGTGG
 CTGGGGACCATGGGATGACCAAAATGGAGACCATGGAGGGGACAGTGAAGTGGAGTCTCAGCTGCTCTCTTTC
 TGTATAGCCCCACAGCAGTCTTCCCCAGCACCCCAACGAGGAGCGAGGATGATTCTCAAGTTAGCCTTGTGG
 CCACGCTGGCCCTGCTGCTGGGCTGCCCATCCCAATTGGGAATATCGGGGAAGTATGGCTGAGCTATTCTCAG
 GGGGTGAGGACTCCCAGCCCCACTCCTCTGCTTTAGCCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGCTGT
 CCCGATTTCTTCATACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT
 TCTCCAAGGCCCTCTGCTGACTACCAAGTGGCTTCTCAGAGCCCCAAGGGGCTGAGGCGACACTCCGCACTGTGA
 TTGCTGAGCTCGACGACTCTCTCGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGGCTCGTTTCTCTCTGGTCC
 GCATGGCGGGGGTACTGCTCTTCTGGCTGCTCTGCTTTATCTGCTGCTGGCATCTGAGCTCAGTGAGCTCATCTCCCT
 CAGGCTTTCCATTCTGCCCTCTACTCCTGACACCTGTGGCTGGGGCTGCTGGTGGGCGCATAGCTATGCTGGAC
 TCCCTGGGAATATTGAGCTGAAGCTAGATCTAGTGCTTCTAGGGCTGCTGAGCTGAGCTCATCTCCCTCT
 TTCTGTGGAAGAGCTGGGCTGGCTGGGGCTCCAGAGGCCCTCGGCAACCTGTTTCCATCCCTGGGCGCCCTCC
 TGTTACTCTGCTGTTTTCGTTTGGCTGTGTTCTTCTGATAGTTTGTGTGAGCTGAGGCGCAGGCCACCCCTC
 TCTTTTGGGCTCATTCCTGCTGCTGCTGTTGTCTCAGCTTCACTGGGAGGGCCAGTGCATTCCACATAAGCTAC
 TCACAAATGCCCGCTTTGGCATCTCAGCCACAACAAACCCCAAGGCCGAGTGGTGCATTCGCCCTGAGGCTGT
 GAAATGGGTTGCTTTTATGTACAGGCTAGCTGGGCTTTTTCATCGTTGCCCTGAAGAGACACCTGTTGCCACT
 CCTCTCGCTGAGTCTGAGTCTCTGGCATCCATGGTGGTGGTGGTCTGAGCCAGAATTTATGGATGGAGCTTGTGG
 CGGCGCTGGTGGCCCTGTGTAGCTGCCGTGGCTTGTGGCTTCGCCGTATGGTAATCTCAAGAGCCCCAGGCCAC
 CCATGCTCTTTGTGGCTGGGACTGCCCTAATGGCATGGGTACTGCTGCCATCTGGCATTTGGCATTTGGCTGG
 CAGATGAGGCTCCCCCGCTCTCCGGCTCTGGTCTCTGGGGCATTCATGGTCTGCCCTGGGCTGTAGCAGGCC
 TGGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTGGTGTGAAGGCTGGGGCAGGCCATCCAA
 GGACCAAGACTGTCTCTACTCCCTCTCAGGCCCCCCACTTCTCAAGCTGACTGGATTATGTGGTCCCTCAA
 TCTACCGACACATGAGGAGGAGTTCCGGGGCGGTAGAGAGGACCAAACTCAGGGTCCCCCTGACTGTGGCTG
 CTATCAGTTGGGAGTGTCTACTCAGCTGCTATGTGTACAGCCCTCACCCTGTGGCCTTCCCACTTCTGCTGT
 TGCATCGGAGCGCATCAGCCTTGTGTTCTGCTTCTGTTCTGCGAGAGTCTCTTCTCTCATCTGCTTGTGCTG
 CTGGGATACCCGTCAACACCCCTGCTCTTTTACTGTGCCATGGCAGCAGTCTCGGCTTGGGCGCTTCTGAGCA
 CACAGACCTCTACTCTCAACAGGCCACAGCCTGTCTTCCAGCCATCCATGGCATGACGCTCTCGTGGGATTCC
 CAGAGGGTATGGCTCTGCTACTTGGCTGCTGCTTTGCTAGTGGGAGCAACACCTTTGGCTCCCCCTCTCTCT
 TTGCACTAGTTTGGCCACTGCTCTGCTGCTGCTGCTGAGAGTCAAGGGCTGGGAAGGACAGCAGCAGC
 CCCCAGGATGAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGGAGCCACTGATGGAGATGCGGCTTCGGG
 ATGCGCCTCAGCACTTCTATGCAGCACTGCTGCAGCTGGGCTCAAGTACTCTTATCTGGTATTCAAGTT
 TGGCCTGTGCTTGGCAGCTCCATCTCTTCTGCGAGCACTCTCATGCTCGGAAGTGTTTGGCCCTAAGTTCTAT
 TTGAGCTTGGGCTCATTGTGAGCAGCGTGGGACTTCTCTGGGCATGCTTGGTGAATGAGTGGATGGTG
 CTGTGAGCTCTGCTTCAAGCACTATTCTGSGCCAGCAGAGCTAGCCTAGTCTGTGATTACTGGCACTTGGCT
 ACAGAGAGCTCGGAGAAGAGTGTAGCTGGCTGTAGAGTACTGGATGATCTCAAGACAGGCTCAGCCATAC
 TCTTACTATCATGACAGCAGGGGCGCTGACATCTAGGACTCATATTCTATATAATCAGGACACAGTGGAGTA
 TGAATCCTAATCTCTGATTGGATGACATCTGAGGGACAGGGGGGCGGTCTCGGAATGGAATAAATAGGCGCG
 GCGTGTGACTTGCACCTATATCCGACACTTTGGGAGCCAGAGGTGGGAGGATTGCTTGGTCCCGAGGATTCA
 AGACCAGCCTGTGGAACATAACAGACCCCGTCTCTACTATTTAAAAAAAGTGTAATAAATGATAATAT

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FIGURE 60

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<subunit 1 of 1, 1089 aa, 1 stop
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MASRFSRVVLVLIDALRFDAQPHSHVPREPPVSLPFLGKLSSLRILEIQPHHARLYRSQ
VDPPTTTMQRKLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLF
PGAFSKAFFFPFSNVRLDLDVDNGILEHLYPTMDSGEWDVLIHFLGVHDHCGHKHGHHPPEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMMTNGDHGGDSELEVSAAFLYSPTAVFPST
PPEEPEVIPQVSLVPTLALLGLPIPFNGNIGEVMAELFSGGEDSQPHSSALAQASALHNAQ
QVSRFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCICLLASQWAI SPGFPFCPLLLTPVAWGLVGAI A
YAGLLGTIELKLDLVLGAVAVSSFLPFLWKAWAGWGSKRPLATLFPPIPGPVLLLLLFLRLA
VFFSDSFVVAERATPELLGSFILLVVLHVEGQLLPKLLTMPRLGTSATTNPPRHNGAY
ALRLGIGILLCTRAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPRLRLVLSGASMLVP
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
EFRGRLERTKSQGPLTVAAYQLGSVYSAMVTALTLLAFPLLLHAERTISLVFLLFLQSFL
LLHLLAAGTPVTTGPPTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWHAAFVGFPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLLPFLCESQGLRKRQPPGNEADARVRPEEEEEEP
LMEMRLRDAPQHFYAALLQLGLKYLFI LGIQLACALAASILRRHLMVWKVFAPKFI FEAVG
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

```

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850, 1016-1034, 1052-1070

Leucine zipper pattern.

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTTGT
 GTCTCTGGTGGTTTGCCTAAACCTGCAAAACATCACCTTCTTATCCATCAACATGAAGAATGT
 CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
 TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTGTGT
 CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA
 TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC
 CAGTGTGTGACCAACCACACGCTGGTGTCTACCTGGCTGGAGCCGAACACTCTTTACTGCGT
 ACACGTGGAGTCCCTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG
 CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTTG
 CCCATATCTATTACCGTGTTCCTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA
 CGTTGGCAAAGAGAAACACCCAGCAAAATTTGATTTTGAATTTATGGAAATGAATTTGACAAAA
 GATTCTTTGTGCCTGCTGAAAAAATCGTGATTAACCTTATCACCTCAATATCTCGGATGAT
 TCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA
 TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAACATTTAG
 GGTATGCTTCGCATTTGATGGAATTTTTTGTGACTCTGAAGAAAAACACGGAAGGTACTTCT
 CTCACCCAGCAAGAGTCCCTCAGCAGAACATAACCCCGGATAAAACAGTCATTGAATATGA
 ATATGATGTGAGAACCCTGACATTTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTTGCAGG
 AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGAGGCAGCGTTGGCAGTCTTGGGCCCCG
 CAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA
 CACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGATCCCC
 AAATGGCAGGCTGTGTATTCTTCGCTGTCCAGCTTCGACCAGGATTAGAGGGCTGCGAG
 CTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGCG
 TCCAGACAGGCCACAGGAGAAAAATGAAACCTATCTCATGCAATTATGAGGAATGGGGGT
 TATATGTGCAGATGGAAAACTGATGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAAC
 AAGTGAGTCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGT
 TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTG
 GTTCATGCATGTAGGTCTCTTAAACATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGT
 GTTCTATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGG
 TGGGTGT

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FIGURE 62

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815

<subunit 1 of 1, 442 aa, 1 stop

<MW: 49932, pI: 4.55, NX(S/T): 5

MSYNGLHQRVFKELKLLTLCSSSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ
CARTLKQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVKGKEKHPANLILYGNFEF
KRFFVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPQSGNLRPPQEEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDKTVIEYEYDVRTTDCAGPEEQELSL
QEEVSTQGTLLESQAALAVLGPQTLQYSYTPQLQDLDPPLAQEHTDSEEGPEEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGDLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEW
GLYVQMEN

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG
TCTGCC**ATG**GGGCTCGGGTTGAGGGGCTGGGGACGTCCTCTGCTGACTGTGGCCACCGCCCT
GATGCTGCCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG
TGACCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA
GGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT
CCGCACTGGCCTGGTGGTCTGGGCGCCACGTCCTGAGTACTGCGGAGCCACCCAGCAGG
TGTTTGGCATCGATGCTCTACCACGCACCCGACTACCACCCCATGACCCACGCCAACGAC
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTGGGCCCTGCAGTGGGGCTGCTGAGGCT
GCCAGGGAGAAGGGCCAGGCCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT
TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGTCCGAGTGCTGGAC
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG
TGGGGACAGCCACAGAGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCTGGTGTGCAGGA
ACCGGGCTCACGGCCTCGTTTCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGAC
GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTCCGGCGAGCAGTCC
CCAGCCCGGCCCTGCCTGGGACCACCAGGCCCCAGGAGAAGCCGCC**TGA**GCCACAACCT
TGCGGCATGCAAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
AAGCCTGATGTTTCAAGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA
AAGGGCAGAAGCAAACCCAGTAAAATGTTAACTGACAAAAAAAAAAAAAAAAAAGAAA

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FIGURE 64

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845

><subunit 1 of 1, 283 aa, 1 stop

><MW: 30350, pI: 9.66, NX(S/T): 2

MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGRF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPQQVFGIDALTTHPDYHPMTHANDIC
LLRLNGSAVLGPVGLLRPLPGRRARPPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLLTLMCTRSGDSHRRGFCSADSGGGLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA

Signal peptide:

amino acids 1-30

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FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCTGACGCTGA
 CGCTGTCCCCGGCCCGGCATGAGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGCACGGTAG
 CAGGCGCCGCCGTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCCAGCAAGGCCACC
 ATCCTTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT
 GGAAGTGGCCAGGAGAGAGAGGCAACATCATCTGGCCTGCCGAGACATGGAGAAGTGTGAGG
 CGGCAGCAAAGGACATCCGCGGGGAGACCCTCAATCACCATTGTCAACGCCCGGCACCTGGAC
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGAGCAAAGATCATTGAAGAGGAGGAGCGAGT
 GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGGACCACCGAGGACGGCT
 TCGAGATGCAGTTTGGCGTTAACCACTGGGTCACTTTCTCTTGACAACTTGCTGCTGGAC
 AAGTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATTGTTGCTGG
 GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT
 GCCAGAGCAAGCTCGCCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGGCTGCAAGGCTCT
 GGTGTGACTGTCAACGCCCTGCACCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG
 CATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCATCTTCTGGCTGTGGTCAAGA
 GCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCCGTGGCGGAGGAAGTGGCGGATGTT
 TCCGAAAGTACTTCGATGGACTCAAACAGAAGGCCCGGCCCGGAGGCTGAGGATGAGGA
 GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCTGGTGGGCTTAGAGGCTCCCTCTGTGA
 GGGAGCAGCCCCCTCCAGATTAACCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG
 ACCGAGGACAGCTGTCCGCCATGCCCGAGCTTCTTGGCACTACCTGAGCCGGGAGACCCAG
 GACTGGCGCGCCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGAGTGGACTGGC
 CTGCAGGTGAGCACTGCCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG
 AGGGGCCATCTGATGCTTCCCCTGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC
 TGTGCATTGACAGGCCAGCTCAGGAGAGCCAGCGGTGCCTGTGCGGGAGGGTTCCAAGGTGC
 TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT
 TGTGCATGCATGGTCCTCTCTGAGCCTTGGTTCTTTCAGCAGTGAGATGCTCAGAATAACTG
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG
 GGTGTTTGTGAGGGCTTCCCTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTATCCC
 GAGTTCAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACCTGGGA
 TTGCTGGGACTCCACCTTCTATCAATTCTCATGGTAGTCCAACTGCAGACTCTCAAAC
 TTGCTCATTT

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FIGURE 66

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop .
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNNARHLDLASLKSIREFAAKIIEEEERV DILINN
AGVMRCPHWTTEDGFEMQFGVNH LGHFLLTNLLLDKLKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGP IFWLLVKPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAEAEDEEVARRLW
AESARLVGLEAPSVREQLPR
```

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTTCGCGAGCGCTGGC**ATGT**GGTCTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG
 GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC
 CAGCGTGGCGCGCGCCCTGGCGCCCGAGCGCGGCTGCTGGGGCTGCTGAGGCGGTACTCTGC
 CGCGGAGGAGGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGGCAT
 GAGGATTCACAACCCCTGTGGCTAACCCCTCTGCTTGCAATTTACTCTCATCAACCGCTGCA
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCCTTTGAGGACCTTGAGGGAGCAGCAAGG
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCCAGGTTGCTTT
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAACGGCTCTTTTCTCTCA
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCCTATGACATGGGGGATATTACCATTGCC
 ATTCATGGCTGGAGGAGGCTGTAGTCTCTTCCGAGGATCTTACGGAGAGTGGAAGACAGA
 GGATGAGGCAAGTCTAGAAGATGCCCTTGGATCACTTGGCCCTTGTCTATTTTCCGGGCGAGGAA
 ATGTTTCGTGTGCCCTCAGCCCTCTCTCGGGAGTTTCTTCTCTACAGCCAGATAATAAGAGG
 ATGGCCAGGAATGTCTTGAATATGAAAGGCTCTTGGCAGAGAGCCCCAACCCAGCTGGTAGC
 TGAGGCTGTATCCAGAGGCCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC
 TATGTCTACACCCTGGGTTCCAGCCCACTCTCTACCAGATCCTTAGCCTCTACTGTTCCTAT
 GAGACCAATTCCAACGCCTACCTGTGCTCCAGCCCATCCGGAAGGAGGTATCCACCTGGA
 GCCCTACATTGCTCTCTACCATGACTTCGTGAGTCACTCAGAGGCTCAGAAAAATTAGAGAAC
 TTGCAGAACCATGGCTACAGAGGTGAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG
 TACCGCATCAGCAAAAGTGGCTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCTCAA
 CCACCGCATTTGCTGCCCTCAGAGGCCTTGATGTCGGGCTCCCTATGCAGATATCTGCAGG
 TGGTGAATATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATTGCTACGTACCAAGC
 AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC
 GGTGGAAGCTGGAGGAGCCACAGCCCTTCACTATGCCAACCTCAGCGTGCCTGTGGTATGGA
 ATGCAGCACTGTTTTGTGGAACTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT
 GCTGGCTGTCTGTCTGTGGTGGGAGATAAGTGGGTGGCCAACAGTGGATACATGAGTATGG
 ACAGGAATTCGCGAGACCCTGCAGCTCCAGCCCTGAAGACT**TGAA**CTGTTGGCAGAGAGAAGC
 TGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA
 AGCAGAGCAGCCCTCTGGAAGAAGGCCTTGTCAGCTTTGCTGTGCCTCGCAAATCAGAGGC
 AAGGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGG
 AGTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTCTGATCAGTGGGT
 TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG
 GGGCTAGCTTGACTCCAGAACTTTAAGACTTTCTCCCACTGCCTTCTGTCTGTCAGCCCAAG
 CAGGGAGTGTCCCCCTCCCAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTT
 TTTAAGTTGAAAACAACCTTTCTTTTCTTTTGTATGATGGTTTTTTTAAACAGTCATTAAAA
 ATGTTTATAAATCAAAA

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FIGURE 68

MGPGARLAALLAVIALGTGDPERAAARGDTFSALTSVARALAPERLLGLLRRYLRGEEARL
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLTGDDCFQ
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPHLQTRDTYEGLCQTLGS
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLLSSVEAGGATAFIYANLSVPVVRNAALFWW
NLHRSGEGSDTLHAGCPVLVGDKWVANKWIEHYGQEFRRPCSSSPED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGGTTTAAGTTCTCTGCTCCATCTCAGGAGGCCCTGCTCCACCCCTAG
GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGAGCCCCGTAACCCGCGCGGGGAG
CGCCCAGGATGCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
TGGCTCAAGTTTCTACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGGCCCTGGTCCT
GTCTGTGGGCATCTATGCAGAGTTGAGCGGCAGAAATATAAAACCCCTTGAAAGTGCCTTCC
TGGCTCCAGCCATCATCTCATCTCCTGGGCGTGTGTCATGTTTCATGGCTCCTTCATTGGT
GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTTCATGTACATCCTTGGGAT
CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCCTTGACCTTCCGGAACAGACCATTG
ACTTCTGAACGACAACATTGGAAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA
AACATCATGGACTTTGTTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG
GAGCAAGAATCAGTACCACGACTGCAGTGCCCTGGACCCCTGGCCTGTGGGGTGCCTTACA
CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAACATATCGAC
AAGGAGCGTTTTCAGTGTGCAGGATGTATCTACGTGCGGGGCTGCACCAACGCGGTGATCAT
CTGGTTCATGGACAACATACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT
TCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC
TCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCCAGCGTGAGGGCGGCAGGCACGGG
ATGCTGCTGTGTGCTACCCCAATTAGGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGGCCCTCTGCCACA
CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCCTGTGTGTAGGTCCCACGGCCTCTGCCTC
CCCAGGGAGCAGAGCCTGGGCCTCCCTAAGAGGCTTTCCCCGAGGCAGCTCTGGAATCTGT
GCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA
GAGCCTGAGGCTCTGCTCAGGGCCCATTCATCTCTGGCAGTGCCCTTGGCGGTGGTATTCAA
GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGG
GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGC
CTCTTCTCAGCCTCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCCTTGAGCCTA
GTTTTTTTTTACGTGATTTTTGTAAACATTCTTTTTTGTACAGATAACAGGAGTTTCTGAC
TAATCAAAGCTGGTATTTCCCGCATGTCTTATTCTTGCCCTTCCCCAACAGGTTTGTAA
TCAAACAATAAAACATGTTTTGTTTTGTTTTTAAAAA

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FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP
AIILILLGVVMFMVSFIGVLASLRDNL YLLQAFMYILGICLIMELIGGVVALTFRNQ TIDFL
NDNIRRG IENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGV PYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDV IYVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN
```

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

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FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCAAGGTCTGGCATCCTGCACCTGCTGCCCTCTGA
CACCTGGGAAGATGGCCCGCCCGTGGACCTTCACCCCTTCTCTGTGGTTTGTCTGGCAGCCACC
TTGATCCAAGCCACCCTCAGTCCCCTGCAGTTCTCATCCTCGGCCCAAAAGTCATCAAAGA
AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC
GTCCCTGAAGCACATCATCTGGCTGAAGGTATCACAGCTAACATCCTCCAGCTGCAGGTGAA
GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
ACACGCCCTTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATC
CGCATGGACACCAGTGCAAGTGGCCCCACCCGCCCTGGTCTCAGTGACTGTGCCACCAGCCA
TGGGAGCCTGCGCATCCAACCTGCTGTATAAGCTCTCCTTCTGGTGAACGCCCTTAGCTAAGC
AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG
ATCGAGGCTTCCCTCAATGGCATGTATGCAGACCTCTGCAGCTGGTGAAGGTGCCCATTTT
CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATT
AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCATAAAC
TCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCGTTCAGCCTCATCGTGAGTCA
GGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCTGTGG
ACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG
GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCAGTT
TTTTATAGACCAAGGCCATGCCAAGGTGGCCCACTGATCGTGTGGAAGTGTTTCCCTCCA
GTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTAC
ACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
GAACCTGTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
ACTCCATCTGCTGCCGAACCAAGAAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTG
AAGGCCTTGGGATTCGAGGCAGCTGAGTCCCTACTGACCAAGGATGCCCTTGTGCTTACTCC
AGCCTCCTGTGTGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG
GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT
CAATAAACACTTGCCTGTGAAAAA

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FIGURE 72

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFITLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQLPLLSAM
REKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITQLYL
GAKLLDSQGKVTKWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGIEASSEAQFYTKGDLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSGVPVSLVKALGFEEAESSLTKDALVLT PASLWKPPSPVVSQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAACATGGCAGCGGTTGGCGGTTTTGGTGTGCTCTGTGACCATTGGTGGTGGCGCTG
 CTCATCGTTTGGCAGCTTCCCTCAGCCTCTGCCCAAAGAAAGAGGAGATGGTGTATCTGA
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAAATGAATGGAGACA
 AGTTCGGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
 CTCCAACTGCATAGACAGTGTGTCTGTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC
 AAACCTCCTGGCGATACTCCAGTGCATTCACCAACAGGATATTTTTGCCATGGTGGAAATTTG
 ATGAAGGCTCTGATGTATTTTCAGATGCTAAACATGAATTAGCTCCAACCTTTCATCACTTTT
 CTGCAAAAAGGGAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC
 TGAGCAGATTGCCCGGTGGATGCCGACAGAAGCTGATGTCAATATTAGAGTGATTAGACCCC
 CAAATTATGCTGGTCCCCCTTATGTTGGGATTGCTTTTTGGCTGTTATTGGTGGACTTGTGTAT
 CTTTCAAGAAGTAATATGGAATTTCTCTTTAATAAAACTGGATGGGCTTTTGCAGCTTTGTG
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCC
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCAGTTTGTGA
 GCTGAAACACACATTGTTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTCTTTTATG
 TGAAGCTGCTACCTCTGACATGGATATTTGAAAGCGAAAGATAATGTGTGTGGCTGGTATTG
 GACTTGTTGTATTATTCTTCAGTTGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC
 CCATACAGCTTTTCTGATGAGTTAAAAAGGTCCCAGAGATATATAGACACTGGAGTACTGGAA
 ATTGAAAAACGAAAATCGTGTGTGTTGAAAAAGAAGATGCAACTTGTATATTTTGTATTAC
 CTCCTTTTTTCAAGTGATTTAAATAGTTAATCATTAAACCAAGAAGATGTGTAGTGCCTTA
 ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAAAATAATTATCCTCTTAACCTTCTCTT
 CCGAGTGAACCTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAAATTGAAAA
 CTACTACTTTGTTTTAGTTAGAACAAAGCTCAAACTACTTTAGTTAACTTGGTCATCTGAT
 TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCTGACCAGGTGTTCCACATATGCC
 TGTTACAGATAAATACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT
 ACTTTACGCATCTTTCCCTTTTGTAGTAGAGAAATTATGTGTGTGATGTGGTCTTCTGAAATG
 GAACACCATTCTTCAGAGCACAGCTCTAGCCCTCAGCAAGACAGTTGTTTCTCTCTCCTCTT
 GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA
 TCTCTAAATACAGGATTATAATTTCTGCTTGTGATGGTGTAACTACCTTGTATTTAGAAA
 GATTTTCAGATTCATTCCATCTCCTTAGTTTTCTTTAAGGTGACCATCTGTGATAAAAATA
 TAGTCTTAGTGCTAAAAATCAGTGAACCTTATACATGGCCTAAATGTTTCTACAAATTAGAGT
 TTGTCACTTATTTCACTTTGTACTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
 CCAGGGCAGTGACTTACGCCGTGAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC
 GAGGTGAGGAGTTCGAGACCATCTGGCCAACATGGTGAACCCCGCTCTCTACTAAAAATAT
 AAAAATTAGCTGGGTGTGGTGGGAGGAGCCTGTAATCGACTACACAGGAGGCTGAGGCAC
 GAGAATCACTTGAACCTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCCTCC
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

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FIGURE 74

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLMWETNKRVPVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFAMVDFDEG
SDVFQMLNMNSAPTFINFFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLMVLLCEAATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

FIGURE 75

AAGCAACCAAACTGCAAGCTTTGGGAGTTGTTGCTGTCCCTGCCCTGCTCTGCTAGGGAGA
 GAAGCCAGAGGGAGGCGGCTGGCCCGGGCGGAGGCTCTCAGAACCGCTACCGGCGATGCTA
 CTGCTGTGGGTGTCCGGTGGTCCGAGCCTTGGCGCTGGCGGTACTGGCCCCGGAGCAGGGGA
 GCAGAGCCGGAGAGCAGCCAAAGCGCCCAATGTGGTGCTGGTCCGTGAGCGACTCTCTTCGATG
 GAAGGTTAACATTTTCATCCAGGAAGTCAGGTAGTGAACCTCCCTTTTATCAACTTTATGAAG
 ACACGTGGGACTTCCCTTCTGAATGCCATACACAACTCTCCAATTTGTTGCCCATCAGCGCG
 AGCAATGTGGAGTGGCCTCTTCACTCACTTAACAGAACTCTTGGAAATAATTTTAAGGGTCTAG
 ATCCAAATTTATACAACATGGATGGATGTCATGGAGAGGGCATGGCTACCGAACACAGAAATTT
 GGGAACTGGACTATACTTCAGGACATCACTCCATTAGTAATCCGTGGGAAGCGTGGACAAG
 AGATGTTGCTTTCTTACTCAGACAAGAAGGCGAGGCCCATGGTTAATCTTATCCGTAAACAGGA
 CTAAAGTCAGAGTGTATGGAAAGGATTGGCAGAATACAGACAAGCAGTAAACTGGTTAAGA
 AAGGAAGCAATTAATTACACTGAACCATTTGTTATTTACTTGGGATTAATTTTACCACACCC
 TTACCTTCACCATCTTCTGGAGAAAAATTTTGGATCTTCAACATTTTACACATCTCTTTATT
 GGCTTGAAAAAGTGTCTCATGATGCCATCAAAATCCCAAAGTGGTCACCTTTTGCAGAAATG
 CACCCTGTAGATTATTACTCTTCTTATACAAAAAAGTGCCTGGAAGATTTACAAAAAAGA
 AATTAAGAATATTAGAGCATTTTATTATGCTATGTGTGCTGAGACAGATGCCATGCTTGGTG
 AATTTATTTTGGCCCTTCATCAATTAGATCTTCTTCAGAAAACTATTGTCATATACTCCTCA
 GACCATGGAGAGCTGGCCATGGAACATCGACAGTTTTATAAAATGAGCATGTACGAGGCTAG
 TGCACATGTTCCGCTTTTGATGATGGGACCAGGAATTAAGCCGGCTACAAGTATCAAATG
 TGGTTTCTCTTGGATATTTACCCTACCATGCTTGATATGCTGGAATTCCTCTGCCTCAG
 AACCTGAGTGGATACTCTTTGTTGCCGTTATCATCAGAAACATTTAAGATGAACATAAAGT
 CAAAAACCTGCAATCCACCTGGATTCTGAGTGAATTCATGGATGTAATGTGAATGCCCTCCA
 CCTACATGCTTCGAACTAACCATCGGAAATATATAGCCTATTCCGATGGTGCATCAATATTG
 CCTCAACTCTTTGATCTTTCTCGGATCCAGATGAATTAACAAATGTTGCTGTAAAAATTTCC
 AGAAATTACTTATCTTTGGATCAGAAGCTTCATTCATTATAACTACCTTAAAGTTTCTG
 CTCTGCTCCACAGTATAATAAAGAGCAGTTTATCAAGTGAACAAAGTATAGGACAGAAT
 TATTCAAACGTTATAGCAAATCTTAGGTGGCACCAGACTGGCAGAAGGAACCAAGGAAGTA
 TGAAAAATGCAATTGATCAGTGGCTTAAACCATATGAATCCAAGAGCAGTTTGAACAAAAA
 GTTTAAAAATAGTGTTCTAGAGATACATATAAATATATTACAAGATCATAAATTATGATTTT
 AAATGAACAGTTTTAATAATTACCAAGTTTTTGGCCGGGCACAGTGGCTCACACCTGTAATC
 CCAGGACTTTGGGAGGCTGAGGAAAGCAGATCACAAGGTCAAGAGATTGAGACCATCTCTGGC
 CAACATGGTGAACCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGCGGTGGTGCACA
 CCTATAGTCTCAGCTACTCAGAGGCTGAGGCGAGGAGATCGCTTGAACCCGGGAGGCGAGCAG
 TTGCAGTGAGCTGAGATTGCGCCACTGTACTCGCCTGGCAACAGATGAGACTGTGCTCGC
 AAAAAAATAAAAAATAAATAATAAATTACCAATTTTTTCATTATTTTGAAGAATGTAGTG
 TATTTTAAGATAAAATGCCAATGATTATAAAATACATATTTTCAAAAATGGTTATTATTTA
 GGCCTTTGTACAATTTCTAACAATTTAGTGGAAAGTATCAAAAGGATTGAAGCAAACTACTGA
 ACAGTTATGTTCCCTTAAATAATAGAGAATATAAAATATTTGTAATAATATGTATCATAAAAAT
 AGTTGTATGTGAGCATTGTAGTGGTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

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FIGURE 76

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885

<subunit 1 of 1, 536 aa, 1 stop

<MW: 61450, pI: 9.17, NX(S/T): 7

MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFDGRITFHPGSQVVKLPIFINF
MKTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDQNTDKAVNW
LRKEAINYTEPFVIYLG LNLPHYPSPSSGENFGSSTFHTSLYWLEKVS HDAIKIPKWSPLS
EMHPVDYYSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY
SSDHGELAMEHRQFYKMSMYEASAHVPLMMGPGIKAGLQVSNVSLVDIYPTMLDIAGIPL
PQNLSGYSLLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS
ILPQLFDLSSDPDEL TNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAI DQWLKTHMNPRAV

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

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FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**
 GCCTCTCTTGGCCTCCAACCTTGTGGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT
 GGTGCCATGCTGCTCCCCAGCTGGAACCAAGTTCTTATGTGCGTGCCAGCATTGTGACAG
 CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG
 TGTGACATCTATAGCACCTTCTGGGCCTGCCCGTGACATCCAGGCTGCCAGGCCATGAT
 GGTGACATCCAGTGCATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA
 CAGTCTTCTGCCAGGAATCCCAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC
 ATCCTTGGAGGCCTCCTGGGATTCAATCCTGTTGCTGGAATCTTCATGGGATCCTACGGGA
 CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG
 GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCC
 CAGAGAAATCGTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC
 TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGT
 ATGTG**TGA**AGAACCAGGGGCCAGAGCTGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG
 CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTCAGAAGGTGCTGCTGAGG
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGCTAGTGTAACAGCATG
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTCTCACCTTGCTGCTC
 CCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG
 ATCCCTTTGCCCTCTGTTTTAGCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTG
 ACTGACCCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG
 GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
 TCCAAGAAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCC
 AGACTAATTTGTGATGAAGTAAATAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG
 GATGCAGGATGGGAGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

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FIGURE 78

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYILGLLGLGLTLVAMLLPSWKTSSYVGASIVTAVGFSGKLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGLLGFIPAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLSLIAGIILCFSCS
SQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

FMP-22 / EMP / MP20 family proteins.

amino acids 46-59

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FIGURE 79

GCAC TGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGC
TTATGTGTCAGTCTGTCTCCTCCTCTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCCCTTTGGCCTCACAAACGATTTTGTTG
TGAAGCTGAAGGTTCAGGGTGTGAATCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTTTCCCTAGAGAAGACATAGAAAGAAAATCAACTTTCAC TAAGGCATC
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

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FIGURE 80

MVPRI FAPAYVSVCLLLCPREVIAPAGSEFWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSE
TRQCGPPCTFWPCFELCCLDSFGLTNDFFVVKLVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:

amino acids 1-25

FIGURE 81

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTT
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA
GTCTGCTTTGAGCAGTGCTGCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGA
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTCAAGTGAACATCAGGGGAA
CGATGACTCCTGGATTCTCCTTCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCACTTCATT
CTGTGACCTGTCTGAGGCCACCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCTCCTGAT
GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAAACCTTCACCCCT
TCTGTGAGATTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTTATGTACTTTATAATGAAAA

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FIGURE 82

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

Signal peptide:

amino acids 1-24

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCGACAGCGCTCACTCGCTCGCACTCAG
 TCGCGGGAGGCTTCCCCGCGCCGGCCGCGTCCCGCCCGCTCCCCGGCACCAGAAGTTCCTCT
 GCGCGTCCGACGGCGAC**ATG**GGCGCTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA
 TCCCTGCTCTTCGCTCTCTTCTCGGTGCGTCCCTAGGTCGGTGGCAGCCTTCAAGGTGCG
 CACGCCGTATTCCCTGTATGTCTGTCCGAGGGGCAGAACGTACCCCTCACCTGCAGGCTCT
 TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
 GCGAGGTGCAGACCTGCTCAGAGCGCCGGCCATCCGCAACCTCAGTTCCAGGACCTTCA
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTG
 GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACCTCGGAGCACAGGGT
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAGATGCACCATCCAACCTGTGTGGTGT
 ACCCATCCTCTCTCCAGGATAGTGAACATCA**CG**GGCTGCAGCCCTGGCTACGGGTGCCTGC
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC
 CTCCAACCGCCGTGCCAGGAGCTGGTGGGATGGACAGCAACATTCAGGGGATTGAACACC
 CCGGCTTTGAAGCCTCACCACTGCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG
 TCCTATGTGGCCACGGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTCGGAGCCCAGCAC
 CCCCCTGTCTCCTCAGGCCCCGGAGACGTCTTCTTCCATCCCTGGACCCTGTCCCTGACT
 CTCAAACCTTTGAGGTCACT**TAG**CCCAGCTGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG
 GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCTCCTTGGCCTCGGCCCTGGTTT
 CCTCCTCTCTGCTCTGGGCTCAGATACTGTGACATCCCAAGGCCAGCCCTCAACCCCTC
 TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTTGGGGTGTGAG
 ATTCTCCCTTAGAGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA
 GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA
 GCATCAGTGGGACAAGATGGACACTGGGCCACCCCTCCAGGCACCAGACACAGGGCACGGTG
 GAGAGACTTCTCCCCCGTGGCCGCCTTGGCTCCCCGTTTGGCCGAGGCTGCTCTTCTGTG
 AGACTTCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCACTGGCCATCGCC
 ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC
 ATATTGGGGCATGGTGGCTCCGTGAGCAAATGGTGTCTTGGCAATCTGAGGCCAGGACAG
 ATGTTGCCCCACCCACTGGAGATGGTGTGAGGGAGGTGGTGGGGCCTTCTGGGAAGGTGA
 GTGGAGAGGGGCACCTGCCCCCGCCCTCCCATCCCCTACTCCCACTGCTCAGCGCGGGCC
 ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT
 GCTATTAATAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

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FIGURE 84

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897

><subunit 1 of 1, 311 aa, 1 stop

><MW: 33908, pI: 6.87, NX(S/T): 6

MGVPTALEAGSWRWGSLFLFALFLAASLGPVAAFVATPYSLYVCPEGQNVTLTCRLLGPDVK
GHDVTFYKWTYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLASD
HHGNFSITMRNLTLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVPSSSQ
DSENITAAALATGACIVGILCLPLILLVYKQRQAASNRRQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

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FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT
 TTCCCCGCGTTCTCTTTTCCACCTTTTCTTCTTCCACCTTAGACCTCCCTTCTGCGCTCC
 TTTCTGTCCACCGCTGCTTCTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCTTTTCGTCTCCCTTCCTCCCGA
 CTCCGCTCCCGGACCAGCGGCTGACCTGGGGAAGGATGGTTCCCGAGGTGAGGGTCTC
 TCCTCCTTGTCTGGGACTCGCGTGTCTGGTTCCCCCTGGACTCCACGCTCGAGCCCGCCC
 AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCCGCGAGAGGTGGCACCCCTACT
 TGGAGCCACAAGGCCTGATGTACTGCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT
 TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATG
 CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACAAAGTCTGCC
 AGCACAACGGGACCATGTACCAACAGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCTCC
 CGCTGCCCAACAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCTCAC
 AACCTGCCCCGAACCAGGCTGCCAGCACCCCTCCCACTGCCAGACTCTGTGTGCCAAGCCT
 GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG
 AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCAGC
 CCCCCTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAG
 GCAGCACAACCTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG
 AAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCGTCGCTTCGGCCCTTGCCTGT
 CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT
 ACCCCTGCGCGTCACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCAGAGGACAAA
 GCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGTCTCT
 CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGG
 CCTCGGACTTGGTGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAAACTGAGGCTCAG
 AGAGGTGAAGTACCTGGCCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA
 AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCAC
 GAAGGTCACTGGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGA
 CAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT
 ATTATATATTAATAAATAAGAAGTTGCATTACCTCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 86

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCFPVHCPQPVTEPQQCCPKVEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFPSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKRGPPTPAPTGLSAPLSFI PRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCIILCTCEDGRQDCQRVTCPT EYPCRHF EKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIY LWKLV
KDEETEAQRGEVPGFRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSDPG
AEGHGQSRQSDQDITKT
```

Signal peptide:

amino acids 1-25

[illegible]

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FIGURE 88

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA
TLQEAATTQENVAWRKNWMVGEGGASGRSP

Signal peptide:

amino acids 1-18

[illegible]

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FIGURE 90

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLLILFLLSWGPLQGQHHLVEYMERRLAALAEERLAQCQDQSSRHAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVVRVPFPWVGTLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLAN
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCIAKLDPQTLDTQEQ
QWDTPCPRENAEAAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

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FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCTCTTCTCTAATCCAT
 CCGTCACCTCTCTGTCTATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGG
 CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
 GGGCCAGACAAGCCTGTCCAGGCCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCTGTCTC
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG
 ACAAACTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAACATTAC
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCA
 TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCTCTCATTTCCATCACGGGATATGTT
 GATAGAGACATCCAGCTACTCTGTCTAGTCTCGGGCTGGTTCCCCGGGCCACAGCGAAGTG
 GAAAGGTTCCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGCC
 TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGAGCATATCCTGTTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTCGA
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
 GCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCAGTGGAATAACAGGCGGAACCTGGAC
 TGGAGAAGAAAGACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACTGTAACCCATA
 GAAAAGCTCCCCAGGAGGTGCCCTCACTCTGAGAAGAGATTACAAAGGAAGAGTGTGGTGGCT
 TCTCAGAGTTTCCAAGCAGGGAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG
 GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG
 ATCATGGTACTGGGTCTCTCAGACTGAATGGAGAACATTGTATTTACATTAATCCCCGT
 TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGGACTATGAGTG
 TGGGACCATCTCCTTCTTCAACATAAAATGACCAGTCCCTTATTTATACCTGACATGTCGGT
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTCTATAATGAGCAAAATGGAACCTCC
 ATAGTCATCTGCCCAGTCAACCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC
 AATCCCAGAGACAAGCAACAGTGAGTCTCTCTCACAGGCAACCACGCCCTTCTCCCCAGGG
 GTGAAATGTAGGATGAATCACATCCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCCA
 GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC
 ACATGGGAGTCAAGTGTCTATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG
 TCAGGAATTTCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA
 AAAAA

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FIGURE 92

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAAFSCFLSPKTNAEAMEVRFFRGQFSS
 VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQK
 AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFPRTAKWKGPQGQDLSTDSRTNRDMH
 GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
 FGIVGLKIFFSKFQWKIQAELDWRKKGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVT
 HRKAPQEVPHSEKRFTRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS
 PDHGYWVLRNLNGEHLTYFTLNPRFISVFPRTPTKIGVFLDYECGTISFFNINDQSLIYTLTC
 RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAIPESTSSESSSQATTFFLP
 RGEN

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGCGCCCGGTGGCGGTGGCGGCGCGGTTGCGGAGGCTTCCTTGGTCCGATTGCA
 ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC
CATGAGGAGCCTGCCGAGCCTGGGCGGCCTCGCCCTGTTGTGCTGCGCCGCCCGCGCGCCG
 CCGTCGCCTCAGCCGCCTCGGCGGGGAATGTACCGGTGGCGGCGGGCGCGGGGAGGTG
 GACGCGTCGCGGGGCCCCGGGTGCGGGGCGAGGCCAGCCACCCCTTCCCTAGGGCGACGGC
 TCCCACGGCCCAGGCCCGAGGACCGGGCCCCGCGCGCCACCGCTCCACCGACCCCTGGCTG
 CGACTTCTCCAGCCAGTCCCCGAGACCACCCCTCTTTGGGCGACTGCTGGACCCTCTTCC
 ACCACCTTTTCAGGCGCGCTCGGCCCTCGCCGACCAACCCCTCCGGCGGCGGAACGCACCTTC
 GACCACCTCTCAGGCGCCGACCAACCGCGCGCCGACCAACCCCTTCGACGACCACTGGCCCGG
 CGCCGACCAACCCCTGTAGCGACCAACCGTACCGGCGGCCACGACTCCCGGACCCCGACCCCC
 GATCTCCCCAGCAGCAGCAACAGCAGCGCTCCTCCCAACCCACCTGCCACCGAGGCCCTC
 TTCGCCTCCTCCAGAGTATGTATGTAAGTCTGTGGTTGGAAGCCTGAATGTGAATCGCT
 GCAACCAGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAACCC
 TGCAAGAGGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTCAGCCATGTGACTGTAGTCC
 ACATGGAGCTCTCAGCATACCGTGCAACAGGTAAGCAACAGAGGGTGAAGTGAAGTTTATT
 TTATTTTAGCAAGGAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG
 GAGGATGAGGGTCATAGATTTTACAAAATATTTTATATACTTTTATCTCTACTTTATATGT
 TATATTTAATGTCAGGATTTAAAAACATCTAATTTACTGATTTAGTCTCTCAAAGCACTAG
 AGTCGCCAATTTTTCTCTGGGATAATTTCTGTAAATTTTCATGGGAAAAATTTATTGAAGAAT
 AAATCTGCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAATGTCTT
 ATGTTTATTAATATACCATTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTTCTCTCTA
 ATCAAAATTTCTACATTTTGTTCTTTGGACATCTAAAGCTTAACTGGGGGTACCCTAATTTA
 TTTAAGTGTGGTAAGTAGACTGGTTTACTCTATTACCAGTACATTTTGGAGACCAAAAG
 TAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTTGGAGTAATTTAATCTAGTGCC
 ATAATGTACTGTTATCTAAGCATTTGCCTTGTACTGCACTGAAAGTAATATTCTTTGACCT
 TATGTGAGGCACCTTGGCTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAT
 AATGAAAAAATAATGACAGGTTATACTCAGTGTAACCTGGGTATAACCCAAGATCTGCTGC
 CACTTACGAGCTGTGTTCCCTTGGGCAAGTAATTTCCCTTCACTGAGCTTGTCTCTCAAG
 GTTGTGTGAAGATTAAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAA
 TTCTGGTTTGTTTAATTTCAAAGGAATATTATGGAAGTGAATGAGAGAACATGTTTTAAGA
 ACTTTTAGCTCCTTGACAAAGAAGTCTTTTACTTTAGCACTAAATATTTTAAATGCTTTA
 TAAATGATATTACTGTTATGGAATATTGTATCATATTGTAGTTTATTAAAAATGTAGAAG
 AGGCTGGGCGCGGTGGCTCAGCGCTGTAATCCTAGCACTTTGGGAGGCCAAGGGCGGTGGAT
 CACTTGAGGCCAGGATTTAGATGAGCCTGGCCAGCACAGTGAACCCCGCTCTACTATAA
 AATACAAACAAATTAGCTGGGCGTGGTGGCACACAGCTGTAGTCCAGCTACTCGGGAGGCT
 GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACT
 GCACCTCCAGCCTGGTGAGAGAGGGAGACTCTGTCTTAAAAA

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FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLSLSLGGALLCCAAAAAASASAASAGNVTGGGGAAGQVDASPGPGLRGEPSPHFFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSFETPLWATAGPSSTTFQAPLGFSPPTTPPAERTS
TTSQAPTRPAPTTLSTTTGPAPTTPVATTVPAPTTPTPTDLPSSSSSVLPTPPATEAPS
SPPEYVCNCNVVGLNVNRCNQTGGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGCGGCGCAGTG TAGACCTGGGAGGA**ATG**GGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG
CCCTGGTACGTGCTTGGCGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGTGGTGGTGACCCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
AGCACGGGCTGGGAGGGTGTGACCAGAGTGT CATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTACCAAGTGGAGCAGGAGC
CTGGGCTTCCTGTCA**AGTAG**CAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAAGAT
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATT
CACAGCA

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FIGURE 96

MGGLLLAAFLALVSVPRQAVWLGRLDPEQLLGFWYVLAVASREKGFAMEKDMKNVVGVVVT
LTPENNLRTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAIIIFTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCTGCC
 CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT
 CCGTGACGGTGACAGGAAGGCCTGTGTGCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT
 GGCTGGATTACCTTGGCCAGTAGTTCATGGCTACTGGTTCGGGAAGGGCCAATACAGA
 CCAGGATGCTCCAGTGCCACAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
 GATTCCACCTCCTTGGGACCCACATACCAAGAATTGCACCTGAGCATCAGAGATGCCAGA
 AGAAGTGATGCGGGGAGATACTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCAACATCCTCATCCCAG
 GCACCTGGAGTCCGGCTGCCCCAGAACTGTACCTGCTCTGTGCCCTGGGCCTGTGAGCAG
 GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC
 CCGCTCCTCGTGCTCACCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC
 AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCCTAC
 CCGCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
 AAATGGCTCATCTCTGTCACTCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC
 TCACAGCCCTCAAACCCGGGGTGCTGGAGCTGCCTTGGTGACCTGAGGGATGCAGCTGA
 ATTACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCGGGGGAGCTGGAGCCACAGCCCTG
 GTCTTCCTGTCTTCTGCGTCACTTTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG
 GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAACCGTGTGAGGGGTTACGCCT
 CTCAGGGGCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCAGCT
 TCTGCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACCCGAGTACTCGGAGATCAAGATCC
 ACAGATGAAGAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCCTCCAGGCAAGGGA
 GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT
 ATGAATTATGTGCAGAGTGAAGACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT
 CCACACTGTGCCCTCCCTTTTATTTTAACTAAAAGACAGACAAATTCCTA

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FIGURE 98

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWF
 REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG
 SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPWACEQGTPPMISWIGTSVS
 PLDPSTTRSSVLTLLIPQPQDHGTSLTCQVTFPGASVTNKTVHLNVSYPQNLMTVFAQDG
 TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
 HLRDAAEFTCRAQNPLGSQQVYLNVSLSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS
 CRKKSARPAAGVGDGTIEDANAVRGASQGPLTEPWAEDSPPDQPPPASARSSVGEDELQYA
 SLSFQMVKPWDSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 99

GACGCCAGTGACCTGCCGAGGTGCGCAGCACAGAGCTCTGGAGATGAAGACCTGTTCTCTG
GGTGTACAGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCTGGAGGAGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCAGGA
AGGTGTCCCGAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCACT
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCTGCTCCACATGGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG
ACTCTCGGAGGAGGACATTTTCACGCCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTAGG
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCTACCACCAGACACAGAGCCCGGACCACCT
GGACCTACCTCCAGCCATGACCCTTCCCTGCTCCACCCACCTGACTCCAAATAAAGTCCT
TTTCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 100

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTGLAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVSFVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

Important features:

Signal peptide:

amino acids 1-17

FIGURE 101

GTTCGCGAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**AT**GAGGATTCTGCAAGTTAA
TCTTGCTTGCTCTGGCAACAGGGCTTGTAAGGGGAGAGACCAGGATCATCAAGGGGTTGAG
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGG
GGCAGCGTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA
TAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGAGGGCTGTGAGCAGACCCGGACAGCC
ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA
CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCGGGCTGGGGCAGCACGTCC
AGCCCCAGTTACGCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCA
GAAGTGTGAGAAGCCTACCCGGCAACATCACAGACCAATGGTGTGTGCCAGCGTGCAGG
AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCACTCTCTT
CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCATCACCCGAAAGCCTGGTGTCTACAC
GAAAGTCTGCAAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA
CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTGTTGGTTTCTGTTCACTCTGTTAAT
AAGAAACCTAAGCCAAGACCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG
CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTGTCTCTGTTATCCCCAGCCCCA
AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 102

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
 <subunit 1 of 1, 250 aa, 1 stop
 <MW: 27466, pI: 8.87, NX(S/T): 4
 MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
 CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
 AVRPLTLSSRCVTAGTSC LISGWGSTSSPQLRLPHTLRCANITII EHQKCE NAYPGNITDTM
 VCA SVQEGGKDCQGD SGGPLVCNQSLQGIISWGDPCAITRKPGVYTKVCKYVDWIQETMKNN

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTTCTGCTGGAGCCGATGCCAAAAACCATGCATTTCTTATTTCAGATTCAATTGTTT
TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA
GTGAAAATAGAAGTTTTGCATCGTCCAGAAAACCTGCTCTAAGACAAGCAAGAAGGGAGACCT
ACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA
CACAAAATGAAGGCCACCCCAAATGGTTTGTTCCTTGGTGTGGGCAAGTCATAAAAGGCCTA
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT
TGCATACGGAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG
AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAGATATTTTAAAGA
AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT
GAACTATAGCATATTTGTATTTCTACTTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA
AAACAAAGTCACTTTTCTCCAAGTTGTATTTGCTATTTTCCCTATGAGAAGATATTTTGA
TCTCCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTGCAACTTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 104

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNHDHGDGFISPKEYNVYQHDEL
```

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

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FIGURE 105

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTCTGCTGAGCCTCTTTGGAGCT
GTGACTCAGAAAACCAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCAGTTCTTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC
CCCGTGTCTACTAAAAATACAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA
TAGTTTCTTGTTCATTTTCGCGACTGCCCTCTCAGTGTTCCTGGGATCCCCTCCCAAATAA
AGTACTTATATTCTC

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FIGURE 106

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHCTCNHGYTSGSGQKLFTFPL
ETCNARHGGSRL

Signal peptide:

amino acids 1-18

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FIGURE 107

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC
AGGGAAAGGGTGACCTCTGAGATTCCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACCCATGG
GGCTCAGCATCTTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC
CAGCCTGCGCTGCGGGGGTGTCCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA
GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG
CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA
CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCCGCTAACCAGCAGCGTTCAAC
CCCTGCCCCTGCCCAATGACTGTGCAACCGCTGGCACCAGTGCCACGCTCTCAGGCTGGGGC
ATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCCTCAACCTCTCCATCGT
CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG
GCGGCTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA
GTCCTTCAAGGTCTGGTGTCTTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG
AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAACTGAC
CTGTTTCTCCACCTCCACCCCCACCCCTTAACCTTGGGTACCCCTCTGGCCCTCAGAGCACC
AATATCTCCTCCATCACTTCCCTAGCTCCACTCTTGTGGCCTGGGAACTTCTTGGAACCTT
TAATCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA
ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
 CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATGT**CGGGCGAGCTCAGCA
 ACAGGTTCCAAGGAGGGGAAGGCGTTTCGGCTTGCTCAAAGCCCGGCGAGGAGGAGGCTGGCC
 GAGATCAACCGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA
 GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAAATGAAGGCGAGATTGACC
 TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG
 AAGATGATCTCAGAGGTGACAGGAGGGGTCAGTGACACTATATCCTACCGAGACTTTGTGAA
 CATGATGCTGGGGAAACGGTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCT**TGA**
 GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT
 CTTGACACACTGTGATCTCTCTCTCTCATTGTGTTGGTCATTGAGGGTTTGTGTTGTTT
 TCATCAATGTCTTTGTAAAGCACAATATCTGCCTTAAAGGGGCTCTGGGTCGGGGAATCC
 TGAGCCTTGGGTCCCCCTCCTCTCTTCTCCCTCCTTCCCGCTCCCTGTGCAGAAGGGCTG
 ATATCAAACCAAAAAGTAGAGGGGCGAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTCCC
 CTCACTTGGAGGAACAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
 ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
 CTGACGGGCTCTTTCGGGTTTCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTACCC
 AGGACACAGCCACTCGGGGCCCCGCTGCCCGAGCTGATCCCCACTCATTCACACCTCTTCT
 CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG
 TACCAGAAGGAACCTCCAGTCCTGTCTCTGCCCACACCTGTGCAGGCAGCTGAGAGGCAG
 CGTGACGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTG
 GGGTTTGGGGGGAAGGTCAGCTCAGTGCTGTTCACCTTTTAGGGAGGATACTGAGGGGAC
 CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
 CTGAGAAATACAAGGTGCTGTGCTGACCCCAATCTGCTTGAAAAA

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FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN
 NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLV
 MFEGKANESSPKPVGPPPERDIASLP

FIGURE 111A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCA
GGAGCGGGGCCCTGACACACCATGGGCCCGGGTGGGCGAGGGGTGCGCGCCGCGCTGCGCGCC
CGCTGCGCGCTGGCCTTGGCGCTGGCGAGCGTCTGAGTGGGCTCCAGCCGTGCGCTGCC
CACCAAGTGTACTCTGCTGCCGTGCCAGCTGGACTGCCAGGGGTGGGCTCCGCGCGGTTC
CTCGGGGCTACCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATACCAGGATC
ACCAAGATGGACTTGCCTGGGCTCAAGAACCCTCCGAGTCTTGCATCTGGAGACAACCAAGT
CAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA
AGAATAAGCTGCAAGTCCTTCCAGAATTGCTTTTCCAGAGCAGCCGGAAGCTCACCAGACTA
GATTTGAGTGAAAACAGATCCAGGGGATCCCGAGGAAGCGTTCCGCGGCATCCACGATGT
GAAGAACC TGAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC
TGCGCGATTTGGAGATCCTTACCCCTCAACAACAACAACATCAGTCGCGATCCTGGTCACGAG
TTCAACCACATGCGGAAGATCCGAACCTCTGCGCCTCCACTCCAACCACCTCTACTGCGACTG
CCACCTGGCCTGGCTCTCGGATTTGGCTGCGACAGCGACGGACAGTTGGCCAGTTTCACTCT
GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCGAGAAGAAGGAGTACCTG
TGCCACAGCCCCCATCGGAGCGCCCATCTCTGCAATGCCAACCTCATCTCCTGCCCTTCGCC
CTGCACTGCGACAATAACATCTGTGACTGTGAGGAAAGGGCTTGATGGAGATTCTCTGCCA
ACTTGCCGAGGGGCATCGTCGAAATACGCCTAGAACAGAACTCCATCAAAGCCATCCTTGCA
GGAGCCTTCACCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA
TATTTGCTCCAGATGGCTTCCAGGGCCTGAATCACTACATCGCTGGTCTGTATGGGAACA
AGATCACCAGGATTGCCAAGGGACTGTTTGTATGGGCTGGTGTCCCTACAGCTGCTCTCTCTC
AATGCAACAAGATCACTCTGCGGGTGAACACGTTTCAAGACCTGCGAGACCTCAAACTT
GCTCTCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCCGCCCTCTGCACT
CCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCGCATGCCACTTGAAGTGGCTG
GCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCGCTGCAAGCAGCCGCGCGC
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCGCGTGCCTGAGGCTCCGAG
ATTACCGCAGAGGTTACGAGCGAGTGTCTTACATGGACCTCGTGTGCCCGAGAAGTGTGCG
TGTGAGGGCACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCCAGCCACTCCC
TGAATATGTACCGACCTGCGACTGAAATGACAATGAGGTATCTGTTCTGGAGGCCACTTGGCA
TCTTCAAGAAGTTGCCAACCTGCGGAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG
CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCAAGT
GGAGACCGTGCACGGGCGCGTGTTCGCTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGA
GTAACCTTGATCAGCTGTGTGAGTAATGACACCTTTGCGGCGCTGAGTTCCGTTGAGACTGCTG
TCCCTCTATGACAATCGGATCACCACCATCAACCTGGGGCCTTCAACACGCTTGTCTCCCT
GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCACTGCCACTGGCCTGGCTGGCGCA
AGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCTAGGTGCCAGAAGCCATTTTCTCTC
AAGGAGATTCCCATCCAGGATGTGCCATCCAGGACTTCACTGTGATGGCAACGAGGAGAG
TAGCTGCCAGCTGAGCCCGCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGGCAT
GCAGCAACAAGGGGCTCCGCGCCCTCCCCAGAGGCATGCCAAGGATGTACCGAGCTGTAC
CTGGAAAGAAACCACTAACAGCCGCTGCCAGAGAGCTGTCCGCGCTCCGACACCTGACGCT
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACTATGTCTC
ACCTCTCCACTCTGATCTGAGCTACAACCGGGCTGAGGTGCATCCCGCTCCACGCTTCAAC
GGGCTGCGGCTCCTCGAGTGTCAACCTTCCATGGCAATGACATTTCCAGCGTTCTCGGAAG
CTCCTTCAACAGCTCAGATCTCTTTCCCATCTGCGCGCTGGGAACCAACCCACTCCAGTGTG
ACTGCACTGTTCCGTTGGCTGTGCGAGTGGGTGAAGGCGGGGTACAAGGAGCCTGGCATCGCC
CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTT
CCAGTGCAAGGGGCGAGTGGACATCAACATTTGTGGCCAATGCAATGCTCTGCCCTCCAGCC
CGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCCCTGCC

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA
GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTAGCTGCTCCTGCCCTC
TGGGCTTTGAGGGGACGGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCCAA
AACAATGCCACCTGGCTGGAGCGGGATCAACAACCTACGTGTGTATCTGTCCGCCTAACTACAC
AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCCTGAGCTGAACCTCTGTGCAGCATG
AGGCCAAGTGCATCCCCCTGGACAAAGGATTACGCTGCGAGTGTGTCCCTGGCTACAGCGGG
AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCAAGTGCCGCCACGGGGCCAGTG
CGTGGACACAATCAATGGCTACACATGCACCTGCCCCAGGGCTTCAGTGGACCCCTCTGTG
AACACCCCCCACCATGGTCCTACTGACAGACCAGCCCATGCGACCAGTACGAGTGCCAGAAC
GGGGCCAGTGCATCGTGGTGACGACGAGGACCCACCTGCCGCTGCCACCAGGCTTCGCCGG
CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAGAGCTCCTACGTGGAAGTGG
CCTCCGCCAAGGTCGACCCAGGCCAACATCTCCCTGACAGGTGGCCACTGACAAGGACAAC
GGCATCCTTCTCTACAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCACGT
GCGGCTGGTCTATGACAGCCTGAGTTCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGA
ATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACAGACCCCTGAACCTAGTAGTG
GACAAAGGAACTCCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG
CCCCCTCTACCTTGAGGGCATCCCCACCTCCACCGGCCTCTCCGCTTGGCCAGGGCACGG
ACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACAGAGTGCAG
GACTTCAAGGCCCTCCCACCACAGTCCCTGGGGGTGTACCAGGCTGCAAGTCTTGCACCGT
GTGCAAGCAGCGGCTGTGCCGCTCCGTGGAGAAGGACAGCAGTGGTGTGCGAGTGCAGCCAG
GCTGGACCGGCCACTGTGCGACAGGAGGCCCGGACCCGTGCCCTGGCCACAGATGCCAC
CATGGAATAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG
GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTACCATG
GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTAGCGGC
GAGCACTGCCAACAAGAGAATCCGTGCCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA
GAAAGTTATGCATCATGTGCCACAGCCTCCAAGTGCCCATCATGGAATGTCTGTGGGGCT
GTGGGCCCCAGTGTGCCAGCCACCCGACAGCAAGCGGCGGAAATACGTCTTCCAGTGCACG
GACGGCTCCTCGTTGTAGAAAGAGGTGGAGAGACACTTAGAGTGCAGGCTGCCTCGCGTGTTC
CTAAGCCCCCTGCCCCGCTGCCTGCCACCTCTCGGACTCCAGCTTATGGAGTTGGGACAGCC
ATGTGGGACCCCTTGGTGATTCAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA
AGAGAAATATTAAGTATATTGTAAAATAAACAATAAATAAGAACTTAAAAAAAAAAAAAAAAA
AAAAA

FIGURE 112

MAPGWAGVGAAVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN
 AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQSVSIERGAFQDLKQLERLRNKNKLQVL
 PELLFQSTPKLTRLDLSENQIQGI PRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL
 TLNNNNISRLVTSFNHMPKIRTLLRHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL
 RGFNVADVQKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
 EIRLEQNSIKAIPAGAFQYKKLKRIDISKNIQISDIAPDAFQGLKSLTSLVLYGNKITEIAK
 GLFDGLVSLQLLLLANKINCLRVNTFQDLQNLNLLSLYDNKLQTTISKGLFAPLQSIQTLHL
 AQNPVFCDCHLKWLADYLDQNPITESTGARCSSPRRLANKRISQIKSKKFRCSGSEDRSRFS
 SECFMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRNDNEVSVLEATGIFKKLPN
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV
 SNDTFAGLSSVRLSLYDNRITITPGAFITLVSLSTINLLSNPFNCNCHLAWLGKWLKRRR
 IVSGNPRCQKPFLLKEIPIQDVAIQDFTCDGNESSCQLSPRCPEQCTCMETVVRCSNKGRL
 ALPRGMPKDVTELYLEGNHLTAVPRELSALRHLLTLDLSNNSISMLTNYTFSNMSHLSTLIL
 SYNRLRCIPVHAFNGRLSLRVLT LHGNDISSVPEGSFNDLTSLSHLALGTNPLHCDCLRWL
 SEWVKAGYKEPGIARCSSPEPMADRLLLTPTHRFQCKGPVDINIVAKNACLSSPCKNNGT
 CTQDPVELYRCACPYSYKGDCTVPINTCIQNPCQHGGTCHLSDSHKGDFSCSCPLGFEGQR
 CEINPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVPELNLQHEAKCIP
 DKGFSCCECPVPGYSKLCETDNDDCVAHKCRHGAQCVDITINGYTCTCPQGFSGPFCHEHPPPMV
 LLQTSFCDQYECQNGAQCIIVVQQEPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRP
 QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHS
 VELVTNLQTLNLVVDKGTPKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
 HGCIHEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVERDSVVECECRPGWTGPLC
 DQEARDPCLGHRCHHGKCVATGTSYMKCAEYGGDLCDNKNDSANACSAFKCHHGQCHISD
 QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRRQKGYASCATASKVPIMECRGGCGPQCCQ
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

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FIGURE 113

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTCCTCCGCA
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT
CCGGCAGGCTTTGAGG**ATGA**AGGCTGCGGGCATTTCTGACCCTCATTGGCTGCCTGGTCACAG
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTCTCGAGGGCTGGCCTG
GACAATTACTGGGGCTTCAGCCTTGGAACCTGGATCTGCATGGCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACTGCCATGTCGCCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTTGTTAAAGA
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGA AAAAAGGCTGTGAGGTTTCCT**TAA**ACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC
GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCTCGTTTCCTCCCAATA
TTCTTCTCAAACCTGGAGAGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT
TTAAATGTC

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FIGURE 114

MKAAGILTIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKLENNHCHVACSALITDDLTDALICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:
amino acids 1-19

FIGURE 115

CAGGCCATTTGCATCCCACTGTCTTGTGTTCTGGAGCCAGGCCACACCGTCCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCCTATTAACCTTGTACATGGCTCCC
 CATTGGTTTTTTGGAGAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTC
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTACTGTCACTTCCAGATCTGCTTCTCAC
 CAAGAGAGATTCTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTACAGCTGCTGTTTTTAAGGAA
 ACATTCAAGTCCCTGTCTCACATAGACCCTGATGTCTCTATCCATCTCTAAATGTCACCAG
 CTTTGACTCAGTTGTTCTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
 CAGCTGCGTGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCCCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
 AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAACAGAAAATCTCC
 CTCCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC
 TCTGGAAGCCATGTACATGCAGTGCCAGTCATTGCTGTTAATTCGGGTGGACCCTTGGAGT
 CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCACTTCTCAGAAGCA
 ATAGAAAAGTTCATCCGTGAACCTTCCTTAAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG
 AGTGAAGGAAAAATTTTCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACCAAC
 TGCTGGTAT**TAA**TCAGATTGTTTTTAAGATCTCCATTAATGTCACTTTTATGGATTGTAGACC
 CAGTTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAAATAAA
 CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA
 AACCATGCTTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG
 TCATTCCATGTTTCAGCAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA
 TAAATTTTGAATGATACATGCGCTTAATGGTTTTTCATAGTTTAAGTGTGTATCATTTATCA
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTAATTGTAGTTCACAGATTCAAT
 CCACCGAAGTGTTCAGTGCATCTGTTAGGGAATTTTTGTTTGTCTGTCTTTGCCTGGATC
 CATAGCGAGAGTGTCTGTATTTTTTTTAAGATAATTTGTATTTTGCACACTGAGATATAA
 TAAAGGTGTTTATCATAAAAAAAAAAAAAAAAAAAA

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FIGURE 116

MPLLLKLVHGSPLVFGEKFKLFTLVSACIPVFRLLARRRKKILFYCHFPDLLLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTFLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPDVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCATGTTGGACTTCGCGATCTT
 CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC
 AAGCTGCAGGAATTCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCTGTGGT
 CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC
 ATATCAATCCCAATAAGACATCGGACCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGTGGCAGTGTGAGTGAAACCACATGAGGAAAAAATTGTATGAAATGGTGT
 GACTGATTCTCTGAAGAGTAACCTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA
 AATGGCTCTCCTA'CCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTGGCT
 ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCTG
 CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAGGCTTTCTAGATGGGTCAC
 TTGATAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAGAACGAAAAGGAAGGAACCTTCAGTCAACATATTTTCATTGACTC
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTAAACCACTCTGAA
 GAAGTTCAAAAAAATTTATATGAAGAGATAAACCAAGTTTTTGGAATGGTCTGTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTGAGCATGTGCTTTGTGAAACTGTCGAACTGCCA
 AACTGACTCCAGTTTTCTGCCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTATTATT
 CCTAGAGAGACCCCTCGTCCCTTATGCCTTGGTGTGGTACTTCAGGATCCTAATACTTTGGCC
 ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTCCCT
 CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGATATATGGTGACCACA
 GTACTTCTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGACAGGTTATTGA
 AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT
 ATTAAATTTTTATACATTTAAATCATTGTTAAATTGATTGAGGAAAACAACCATTTAAAAA
 AAATCTATGTTGAATCCTTTTATAAACCAAGTATCACTTTGTAATATAAACACCTATTGTAC
 TTAA

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FIGURE 118

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
 ERYGPVVSFWFGRRLLVVSILGTVDVLKQHINPNKTSDFPFTMLKSLLRYQSGGGSVSENMRK
 KLYENGVTDSLKSINFALLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
 DDQEVIRFQKNHGTVMWSEIGKGLDGS�DKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
 QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTSEEVQKKLYEEINQVF
 GNGPVTPEKIEQLRYCQHVLCETVVRTAKLTPVSAQLQDIEGKIDRFIIPRETLLVLYALGVVL
 QDPNTWPSPHKFDPRFDEDELVMKTFSSLGFSGTQCEPELRFAYMVTTVLLSVLVKRLHLLS
 VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

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FIGURE 119

CTAGATTTGTCGGCTTGCAGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCAGCCTCAGA
GACCGCCGCCCTTGTCCCGAGGGCC**ATG**GGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC
CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT
ACAGGCCTGCCTGCCTCTCACGTTCAACCCCGAGGAGTATGACAAGCAGGACATTAGCTGG
TGGCCGCGCTCTCTGTCACCTTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA
GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT
GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACTACGTATTGGTACATTTTTGTCT
TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTTCGTCAACCGTCTTTGGGCTGAAA
AAGAAACCCCTTCT**TGA**TTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG
CCGCTTCGTATTCTGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTC
TGCTGGAGGATATGTGTTGGAATAATTACGCTCTTGAGTCTGGGATTATCCGCATTGTATTTA
GTGCTTTGTAATAAAAATATGTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA
ATTAAAAAAAAAAAA

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FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
 LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVT
 EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

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FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACT
 GACTCGCTGCTGCTTCTGTTCTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
 ATGATGGTCTCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC
 CGGGTGCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCT
 CCTAGGGCTGCTGGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC
 CGAACCACAGCCCCCACCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTACAGGGAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCACCAGGAACAGCAGATCTTCATCGAAGCCAAG
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCCGCGGACCTC
 GCCTTTCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT
 GGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCAGGACTAT
 CGGCTGGTCCAGAAGGTGTGCCCAGATTACAACTACCATAGTGATACCCCTTACTACCCTATC
 TGGGCTGAACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTTGAAGGACAGGCCTGCCCATGC
 AGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGCCCTCAGGCAGGGAGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG
 CTGGTCCCAACCTGAAGCTGTGGAGTGAAGTACATCAGGAGCACTGGAGGAGGAGTGGGCT
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCGAGGCC
 TGTGGGCAGGCCGATCAGTGTGGCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTCATCAGTGTGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCTTGTCTGTGTCTGAGCATG
 GCATGAGGCTGAAGTGGCAACCTGGGGCTTTGATGTCTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGACACCCATT
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCC
 ACAGCCCATCCGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG
 CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTCTCC
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCAGGGTGGGGCGGGGCCGGCCGAGA
 GCATGTGCTGGATCTGTCTGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGT
 GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTCTTGGAGCAGGAATAAAGCTT
 GCCCGGGGGCA

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FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

MQLTRCCFVFLVQGSlyLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPY
YPSG

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCA
 GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGTTCTGCATGAGCTCCTTAAAG
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT
 TGGTGGAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG
 CATCTTCCCGAGCACCGGGATCCCGGGGTAGGAGGCGACGCGGGCAGCACCGCCAGCC
 GGCTGCGGCTGCCACACGGCTCACCATGGGGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG
 GCCGTGCTGCTGGTCTCTACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC
 CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG
 GTCCTCTTCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCTTCTCG
 GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT
 CGATCAGATCCTGGTGAATGTGGTAATTTTTTTCATTGGAGTCTGTCTTTGTAGCACCAA
 GAAAGGAATTTACAGTTTCAGTTTTTCACGTGATTAAGTCTACCAGAGCCAAACTATCCAG
 GTTAACCTTGATGTTAAATGGAAAACCAGTAATATCTGCCTTTGCGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGTCTGTCTACCTAGATAAAGAGGATAAGGTTTACCTAA
 AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATTCACGTTTTCTGGCTTCTGGTG
 TTCCCCCTATAGGATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG
 AGTTATTGGAAGATCATTTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG
 GATATGGATTCTAAGGATTTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG
 TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA
 ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTCAATTCCTGGGATTACTGAATTAGT
 TACAGATGTGGAATTTTATTGTTTAGTTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AAACCTCAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAGAAGCTGATACTG
 TGTTAATATATTGATTATTTGTTTATTTTATTCCTTTGGAAATGATTTTGTTGGTTCTTGTA
 AAAACTTGGATTTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTAAAATAAGGTAATGAA
 TGGCTTGCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAAA
 GAATGCTTCATAGTTGTATTTTAATGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT
 TTCTAAGAAGAAGAATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCCCTCCGAGGGAAATCTTATACTTTATTGC
 TCAACTTTAATTAATAATGATTGATAATAACCACTTTATTAATAAACCTAAGGTTTTTTTTTT
 TCCGTAGACATGACCACTTTATTAACCTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT
 TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCGCTTAACCTCTTAAATTTGA
 TATATTTATCTGTTTAGCTAATATTAATTCAAATATCCCATATCTAATTTAGTGCAATAT
 CTTGTCTTTTGTATAGGTCAATGAATTCATAAAATATTTATGTCTGTTATAGAATAAAGA
 TTAATATATGTTAAAAAA

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FIGURE 126

MGSGRRALSAVPAVLLVLTLPGLPVWAQNDTEPIVLEGGKCLVVCDSNPATDSKGSSSSPLGI
SVRAANSKVAFS AVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESVVFVAPRKGIIYSFSF
HVIK VYQSQT IQVNLMLNGKPVISAFAGDKDVTREATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

FIGURE 127

CGGTGGCC**ATG**ACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC
GCCCTTTATGCTTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC
TTTCTTCTGGTTGGTGTCTCTACTGATTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTA
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC
TATATCCAAGAAATGTTCCGATTGTCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAACCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG
CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCCTTTATTTCAGCTTTTCATGAC
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGTATGGCTGTGAGAAGA
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGTCTATGGGCAC
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTGACCTGCTCTGCCAAG
ACAAGAAGTTTCTTCTTTACAACCAGCGCTCCAGAT**TAA**CCCTCAGGGAACAGCACTTCCCAA
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTTCTG
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

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FIGURE 128

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop .
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLGPGTVGIHGDSPOFFLYSAFMTLVIIILHVFWGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKLCLLCQDKN
FLLYNQSR

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

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FIGURE 129

CGGCAACCAAGCGCCGCCACACCGCTGCCACTGCCGCCCTGCCGGGGCCATGTTGCTCTGGGCTTGCCCTTCT
 TGGTGCTCTTGGTGGCTCGGTGCGAGGCCATCTGGGGGTTCTGGGGCCCAAGACGCTCTCGCAGAAAGACGCGG
 AGTTTGAGCGCACCTAGCTGGACGAGGTCAACAGCGAGTGGTCAACATCTACACCTTCAACCATCTGTGACCC
 GCACAGGACAGAGGGCGTGGCTGTCTGTGAACGTCCTGAACAGCAGAGGGGGCGCGTGTGCTTTGTGG
 TCCGCCAGAGAGGGGTGTGGTGCTTCCAGGTGCCCTAATCTCGAGGGATGTTTCAGCGCAAGTACCTCT
 TCCAAAAGGTGAACGACACCTGTGTGACGCCCCACCAAGATGAGTCGGAGATTCAGTTCTCTACGCTGGATG
 AGTCCACCTGTCCACAGTCAACACCAATACCAAGCTCCGGGTACGCCGATGGACGATTTTGTGCTCAGGACTG
 GGGAGCAGTTGAGTCTCAATACCAACAGCAGCAGCCGAGTACTTCAAGTATGAGTTCCCTGAAGGCGTGGACT
 CGGTAATTGTCAAGGTGACCTCCAACAGGCCCTTCCCTGCTCAGTCATCTCAGTACAGGATGTGCTGTGCTCTG
 TCTATGACCTGGACAAACAGTAGCCTTCATCGGCATGTACAGACGATGACCAAGAGGGCGGCCATCCCGGTAC
 AGCGCAAGACTTCCCCAGCAACAGCTTTTATGTGGTGGTGGTGAAGACCAAGACCAAGCTCAGCGGGGCT
 CCTGCTCTTTACCCCTTCGCAAGATGAACCGGTGATCAAGGGCACC GCCAGAAAACCTGTGAGTGTGG
 TGTCTCAAGCAGTCACGCTGAGGCATACGTCAGTGGGATGCTTTTGCTGGGTATATTTCTCTCCTTTTACC
 TGCTGACGCTCTCTGGCTGCTGGGAGAACTGGAGGCAGAAAGAACCCCTGCTGGTGGCCATTGACCGAG
 CCTGCCCAGAAAGCGGTCAACCCTCGAGTCTTGGCTGATTTCTTCTGGCAGTTCCTCTATGAGGGTTACAAC
 ATGGCTCTTTGAGAAATGTTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCACTGGGGGACTCTCTTACG
 GTTACCAGGGCCGCTCCTTTGAACCTGTAGGTACTCGGCCGAGTGGACTCCATGAGCTCTGTGGAGGAGGAT
 ACTACGACACATGACCGCATCGATTCCGACAAGAAATGTATTCGCAACCAAGCAATACCTCTATGTGGCTGACC
 TGGCAGCCAGGAGCAACGCTGTTTTCGGGAAAAAGTACCAAGTCTTGTGAAAGTATGGCAACCTTGTCTGTCT
 TCTATGACCTTCTGTGGTGACGCTGGTGATCACTACCAAGCGGTGGTGAATGACAGGGAATCAGGACATCT
 GCTACTACCAATCTCTCTGCGCCCAACCTGCGGCAATCTCAGCGCTTCAACCAACCTCTCAGCAACCTGGGGT
 ACATCTCTGTGGGCTGCTTTTCTGCTCATCTCTGCAACGGGAGATCAACCAACAGCGGGCCCTGCTGCGCA
 ATGACCTCTGCTGGCTGGAATGTGGGATCCCAAAACACTTTGGGCTTTTCTACGCCATGGGCAAGCCCTGTAGTA
 TGGAGGGGCTGCTCAGTGCTTGCTATCATGTGTGCCCAACTATACCAATTTCCAGTTTGACACATCGTTTCATGT
 ACATGATCGCGGGATCTGATGCTGAAGCTTACCCAGAGCGGCCACCCGACATCAACGCCAGCGCTCAGATG
 CCTACGCTGCTGGCCATTGTGATCTTCTCTGCTGTGCTGGCGTGGTCTTTGGCAAGGGAACACGGCGTTCT
 GGATCGTCTTCTCATATTACATCATCATCGCCACCTGCTCCTCAGCAGCGAGCTATTAGATGGGCGGTGGA
 AACTGGACTCGGGGATCTCCGCCGACCTCCACGCTGCTTACACAGACTGCATCCGGCAGTGACGCGGGCGCG
 TCTACGTGGACCGCATGGTGCTGGTCATGGGCAACGTATCACTGGTGGCTGCCATGGGCTTATCA
 TGCGCCCAATGATTTCGCTTCTACTTTTGTGGCCATGGCATCTGCAACCTGCTCCTTTACTTCGCTTCTACA
 TCATCATGAAGCTCCGGAGTGGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATGTTTGACCTCCGTGGTCT
 GGGCTCTGCGCTCTTCTTCTTTCAGGGACTCAGCACCTGGCAGAAAACCCCTGCGAGTTCAGGGAGACCA
 ACCGGGACTGCATCTCTCTCGACTTCTTGACGACCAGACATCTGGCACTTCCCTCTCTCCATGCCATGTTTCG
 GGTCTTCTGGTGTGCTGACACTGGATGACGACTGGATACTGTGACGGGACAAGATCATGTCTTCTAGC
 AGGAGCTGGGCGCTTCTGCTCACTCAAGGGGCCCTGAGCTCCTTTGTGCTATAGACGGCTCACTGTGCTGTCT
 GTGGGATGAGTCCCAAGCCCGCTGCCAGCACTGGATGGCAGCAGGACAGCGTCTAGCTTAGGCTTGGCTCT
 GGGACAGCATGGGCTGGATGGAACCTTGACGCTGCCCTCTGCGGAGGACAGGCTGCTCCCTGGCAACCC
 AGATGTTGGGCAAAATGCTGCTTTCTTCTCAGTGTGGGGCTTCCATGGGCGCCCTGCTTGGCTTCTCAATTT
 TGCTTTTGCAGAGGAAGGATGGAGGGACACCTTCCCAATTCATGCTGCATTTGCGCGTCTCTCTCC
 ACAATGCCCGGCTGGGACTTAAGCGCTCTTTTCTCCCATCTCCCACTCCAGGGCTAGCTGGGGCGTGA
 ATCTCTGTCTGTATCAGGGCCCACTTCTCTTTGGGCTGTCCCTGGCTGCCATCTGAGCAATGCGCTCAGCAGCC
 AGGATGGATGGGGGTATGAGATTTTGGGGGTTGGCCAGCTGGTGGCAGACTTTTGTGCTAAGGCTTCCAAAGGG
 CTGGGGGCACTGGTATTCTTCTTCCCTGACCTTACGGCTGGCTCTTTCAGGAGCTGCTCAGCCCAAT
 TGACAACCGCTTCTGATTCAAGAGGCTGAATTCAGAGGTCACTTCTATCCCATCAGCTCCAGACTGATGCC
 AGCAGCAGGACTGGAGGGAAGCGCTCACCCCTTCCCTTCTTTCAGGCGCTTGTCTTGGCAACCC
 AGCTGGTGGCTTCTCAGTGCAATGACACTGCCAAGAAATTCAGAGGGGCAAGGAGGATATACAGATTCAG
 CCGCTTCTGCCCTCAGAGTGTGGGCGACCCGAGCTACCTTACGAAGGGGCTTCAGGAAGGATGTGCTGTT
 CCTCTACGTCGCGCTGCTAGCTCTGCTTCTAGGACCGAGGCTGGCTTCTAGTTTTCGCTCAGCTCTCAGCA
 AGTTCTGTGTAGTACTGCACACATACCTATGAACCTTGGAGTTTACGAAGTATGCCCACTCTGGGCA
 CCGGGCCACCTGTGCTCTGGATGCCCTTCTGCCACCTGGTCCACCCAGATGTGCTGAGGATGGGAGCTCAGG
 CTGGGCTCTGCTTTGGGATGGGAATGTGTTTTCTCCCAACTGTTTTATAGCTCTGCTGAGGGCTGGG
 AGATGAGGTGGGTCTGATCTTTCTCAGAGCGTCTCCATGCTATGGTGCATTTCGTTTCTATGAATGAAT
 TGCATTCAATAAACACAGACTCAAAAAAAAAAAAAA

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FIGURE 130

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHGLVGLPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRGTGEQFSFNTTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFCPSVISIQDVLCPVYDLDNVAFIGMYQTMKKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFYPPFAEDEPVDQGHRQKTL SVLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLVAIDRACPESGHPRLVADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDL SYGYQGRSFEPVGT RPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVL RKKYQIYFWNIATIAVFYALPVVQLVITYQT VVNVTGNQDICYNFLCAHPLGN
LSAFNNILSNLGYILLGGLFLLIILQREINHNRALLRNDLCALECGIPKHFGLFYAMGTALM
MEGLLSACYHVCPTYNTNFQFDT SFMYMIAGLCMLKYQKRHPDINASAYSAYACLAIVFFS
VLGVVFGKGNTAFWIVFSIIHIIATLLSTQLYMGWRWKLDSGIFRRILHVLYTDCIRQCSG
PLYVDRMVLVLMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFFQGLSTWQKTPAESREHNRDCILDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF

```

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCCTGCGCTTGCCCCACCCAGGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTTGGGCGCTGGAGGGCGTGCTCTG
 ACC**ATG**GTCCCTGCGCTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGC
 CCAGCTGGCAGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGAAAAATTTCCCTTTATACC
 TGACCAAGTTGCCGCTGCCCGGTGAGGGGGCTGAAGGCCAGATCGTGCTGTACAGGGGACTCA
 GGCAAGGCAACTGAGGGCCATTGTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGAGCAG
 GGCCCTGGACCCAGAGGAGCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATG
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAAGGTG
 CCCCATTTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCTTGGCATCCC
 CTTCTCTTCTCTTGAAGGCTTACAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT
 TCCACATCCTGAGCCAGGCTCCAGCCAGCCTTCCCCAGACATGTTCAGCTGGAGCCTCGG
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC
 CTACAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG
 CCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA
 GAGATCTCAAAGTCTTATACCCGACCCACATGGGCCAGGTACACTGGAGTGGGGGTGATGT
 GCATATCACCTGGAGAGCCATCCCCCGGGACCCTTTGAAGTGAATGAGAGGGAACTCTCT
 ACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
 AATTTCCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA
 TGACAACGTCCTATCTGCCCTTCCCCGTGACCCACAGCTCAGCATCTCTGAGCTCAGTCCAC
 CAGGTACTGAAGTGACTAGACTGTGCAGCAGAGGATGCAGATGCCCGCGCTCCCCCAATTTCC
 CACGTTGTGTATACGACTCTGAGCCCTGAGCCTGAGGATGGGGTGAAGGGAGAGCCCTTCCA
 GGTGGACCCCACTTACAGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACAA
 TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT
 GAAGTCGAAGTCGCAGTACAGATATCAATGATCACGCCCTGAGTTTCATCACTTCCAGAT
 TGGCGCTATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCA
 TTGATGCTGACCTCGAGGCCCGCTTCCGCTCATGGATTTTGCCATTGAGAGGGGAGACACA
 GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGACAGATGTGGCGA
 AGCTGGTGGGGCCAGGCCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA
 GTGATGCCACCCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCC
 AGCCGGCTCTTCTGCTGACCATCCAGCCCTCCGACCCCATCGCGAACCCCTCAGGTTCT
 CCTTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTTCCGGGGAGGTTGCACACC
 GCCCAGTCCCTGACAGGGCGCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCCAGGA
 TACAGCCCTGACTCTTGCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAAGCATG
 GCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCAGGTCCTCAGAC
 TTCACCTTTGGTCCCAACCCACGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTC
 CCATGCCCTACCTTACCTTGGCCCTGCATTGGGTGGAGCCAGCTGAACACATAATCCCGGTGG
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGTGCTGCAAC
 GTGGAGGGCAGTGCATGCGCAAGGTGGGCCGATGAAGGGCATGCCACGAAGCTGTGCGG
 AGTGGGCATCCTTGTAGGCACCTGTGTAGCAATAGGAATCTTCCTCATCTCATTTTACCC
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCTGAAGGCG
 ACTGT**TGA**ATGGCCCCAGCGCTTAGCTGGGAGCTTGGCCTTGGCTCCATCTGGCTGCC
 CTGGAGAGAGGCCACGCCAACAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCTCTGCT
 CTGCCCTGGGGTGAGGCACCATCACCATCACAGGCATGTCTGCAGAGCTGCACACCAAC
 TTTATGGACTGCCCATGGGAGTGCTCCAAATGTACGGGTGTTTGCCCAATAATAAAGCCCCA
 GAGAAGTGGGCTGGGCCATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

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FIGURE 132

MVPAWLWLLCVSPQALPKAQAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
 KATEGPFAMDPDSGFLLVTRALDREEQAQYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP
 HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSPDMFQLEPRL
 GALALSPKGSTSLDHALERTYQLLVQVKMDGDAQSGHQATATVEVSIESTWVSLEPIHLAE
 NLKVLYPHHMAQVHWSSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQN
 SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH
 VVYQLLSPEPEDGVEGRAQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGFSSTCE
 VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTADLEPAFRLMDFAIERGDTE
 GTFGLDWEPPDSGHVRLRLCKNLSYEAAPSHEVVVVVQSVAKLVGPGPGPGATATVTVLVERV
 MPPPKLDQESYEASVPISAPAGSFLLLTIQPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTA
 QSLGQAQPGDITYTVLVEAQDTALTALPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
 TLGNPTVQRDWRLQTLNGSHAYLTLALHWVEPREHIIPVVVSHNAQMWQLLVIVCRCNV
 EGQCMRKVGRMKGMPTKLSAVGILVGTLVAGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA
 GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
 ATTGAGTCAACTAGTGAATTCAAACAACCTGAAGCTCAATTTCTGGAATCTCCTCTCCTCT
 TCAATCGGCTGTGGATGTCTGGTCCCATCTGTCACTCTGCAGGCAATTTAAATPCTTCTCTG
 AGATCCCAGGGCTTAGAGTACGCACTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA
 AGATGATGAAATGCAACCAATGAAGGCAAGAACGGAGCAGTAATAACTTCAACTACCGGGG
 CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCCTGAC
 CTGGCGAGGAGGGTGAAGATTGGACATTCGTTTGAACACGGGCCGATGTATGTACTGAAGTT
 CAGCACTGGGAAAGCGTGAAGCGGCCGCCGCTTTGGCTGAATGCAGGCATCCATTCCCGAG
 AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAAGAG
 GATCCAGCTATCACCTCCATCTTGGAGAAATGGATATTTTCTTGTGTGCCTGTGGCCAACTCC
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGGCTGCCGAAATC
 CTGGAAGCTCCTGCAATTTGGTGTGACCCAAATAGAAACTGGAACCGTAGTTTTGCAGGAAAG
 GGAGCCAGGCACAAACCTTGTCTCGAAGTGTACCATGGACCCACGCCAATTGCGAAGTGGA
 GGTGAAATCAGTGGTAGATTTTCATCCAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC
 ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCACTAGTCAAAAAGGCCCGACATGCC
 GAGGAACTCGACAAGGTGGCGAGGCTTGGCGGCCAAAGCTCTGGCTTCTGTGTGGGCACTGA
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG
 CGTATGACAAACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGC
 TTCTCCTGCCAGCTAACCAAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC
 CATCATGGAGCATGTGCGGGACAACCTCTACTAGCGGATGGCTCTGCTCTGTCTACATTTAT
 TTGTACCCACACGTGCACGCACCTGAGGCCATTGTTAAAGGAGCTTTTCCCTACCTGTGTGAG
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCTCGGAGT
 CGTGTGTCTGGCGGTGTCCTTGCAAGAACTGGTTCTGCCAGCTGCTCAATTTTGGTCTCTG
 CTGTTTTTGATGAGCCTTTTGTCTGTTTCTCTCTCCACCCTGCTGCTGGCGGGTGCACCT
 AGCATCACCCCTTCTGGGTGGCATGTCTCTCTACCTCATTTTTAGAACCAAGAACATC
 TGAGATGATTCTCTACCCTCATCCACATCTAGCCAAAGCCAGTGACCTTGTCTCTGGTGGGCA
 GTGGGAGACACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCTTTAATTTT
 TCGCAGTCTTCTTGAAAAATATTTTCCCTTGAGCAGCAAACTCTTGAGGGATATCAGTGAAG
 GTCTCTCCCTCCCTCCTCTCTCTTTTTTTTTTTTTTGTAGACAGAGTTTGTCTTGTGTGCC
 CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCAACCTCTGCCCTCGGTGTCAAGCA
 ATTCCTCTGCCCTCAGCCCTCTTGAGTAGCTTGGTTTTATAGGCGCATGCCACCATGCCCTGGCTA
 ATTTTGTGTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAAGCTGGTCTCAAACCTCCCA
 ACCTCAGGTGATCTGCCCTCCTTGGCCCTCCCAAGAGTGTGGGATTACAGGTGTGAGCCACTG
 TGCCGGGCCCGTCCCTCCTTTTTTAGGCCGTAATACAAAGTAGAAGATCACTTTCCTTCAC
 TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTTATTCAGTGTG
 ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGTACTGTGCCAGGAGGCTGGCTGGA
 GTGACCATCTAAATTCAGGATGGTGAATTTATCCCCATCTGTCTTAATGGGCTTACCTCCT
 CTTTGGCTTTTGAACCTCACTCAAAGATCTAGGCCCTCATCTACAGGTCCTAAATCACTCAT
 CTGGCCCTGGATAATCTCACTGCCCTGGCACAATTTCCATTGTGCTGTGGTGTATCCTGTGTT
 TCCTTGTCTGGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
 TCTGTCTAATTTTGTATCCTGGACCACAAGTTCCCTAAGTAGAGCAAGAATTATCAACCAAGCT
 GCCTCTGTTTTCATTTCACTCAAGCAGCTACCATCTGTCTCTTTGTTGTGTGTGTGTGTGTGT
 TTGTTTTTGTCTTTTACCAAAACATGTCTGTAATCTTAACCTCTGCCTAGGATTTGTGTA
 GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCATGTGAAAAAAAAAAAAAAAAAAAA

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FIGURE 134

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFN
PVDVLVPSVSLQAFKSFRLSQGLEAYVTIEDLQALLDNEDEMQHNEGQERSNNFNYGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRPAVWLNAGIHSREWI
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNLWRKTRSRNPGS
SCIGADPNRNWNASFAGKGASDNPCSEVYHGHANSEVEVKSVDVFIQKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAALKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLLPANQIIPTAETWLGLKTIMEHVRDONLY

Signal peptide:

amino acids 1-16

[illegible]

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FIGURE 136

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIIHQGFQHLVHSLTVP
SKDLTLKMGSALFVKKELQLQANFLGNVRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGG
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMHQKEQFAF
GVDTELNCFLVQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATT
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

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FIGURE 138

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVSSGASTATNSGSSVTSSGVSTATI
SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE
SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS
TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT
SNGAGTATNSESSTTSSGASTATNSDSTVSSGASTATNSESSTTSSGASTATNSESSTSS
GASTATNSDSTSTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA
NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSTTSSEAST
ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV
SEAKPGGSLVPWEIFLITLVSVVAAGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP
GPGGNHGAHRPRWSPNWFRRPVSSIAMEMSGRNNGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
CCAGCAAT**ATG**CATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
CTGTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGC
ATGCCGGAAGGGAAAGTGGAGAAGGTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC
AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCACACTGGGGTCCAC
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGTCAACCATGCTGCTGACCAGGCTGG
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCACAACCACGCCGTTAGCCTCTGG
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG
GGCCTCAGTCAACACGCCTTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA
TGCCCT**TAA**ACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCAATCAGCTGAC
ATGACCTGGAGGGGTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG
GGATTTGTGAATAAACTTGATACACCA

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FIGURE 140

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop .
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHTKELDRGVQGLNHGMDKVAHEINHIGQAGKEAEKLGHVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

FIGURE 141

TCCGGGTTCCCGAGGGGCTTCGCCGCGCGGCTTGGCAAGGGGACGAGTCAGTGGACATCCAGGAAGACGGCG
 CGCGCGGGGGGACATGACCTGCTGCGCTGACCGCTGACTACTCTACGAGGCGCGGGGCCCCGGGGGACGCTG
 GGGGCGGACCGGGGGCGGAGCTCGCGCCGCTGAGTCTCGGCCGAGCCACTCTGAGCCGCGAGCGGGGACACCTGCT
 GCTCTGTGCTTCTCGGAAGTCTGCGACAGGACTGGGCTCTGAGGAGCTTGGCTCGGCCCCACTGGGGGCGCTGTGCC
 CTTGCGGCACCGCTGTCTGCTCTCTGCTCTGCTGCTCTCTGCTGACGGCCGCGCTTCCAGCTTGGGCGCTTACG
 CCCCCGATCAGCTTGTCTTGTGGCTTCTGAAGAGCGGCCATCTTCAGATTTCGAGCTTGAACACATCTCCAACTAC
 ACAGCGGCTTCTGCTGAGCAGGGTGGCAGGACGCTGTAGCTGGGTGCTGACAGGCCCTCTTTCAGCTACGTAGTAC
 AACTCAGCTTCTCTCGCAGGGGGAGTACAGGAGTCTGCTTTGGGTGTGACAGCAGAGAAACAGACATGTC
 AGCTTCAGGGCAAGGACCCACAGCGGCACTCTCAAATACATCAAGATCTCTCTCGGCTTACCGGCAGCTAC
 GTCTTCACTCTTGGCAGCAGCTTTCAGCCCATGTGTACTACATCAACATGGAACTTACCCTTGGCAAG
 GACGAGAGGGGAATTCTCTCTGGAGATTGGCAAGGAGCTTGTCCCTTGCAGCCGAATTCTCAAGTCCAGCTCTCC
 TGGTGGTTGTATGGGAGCTTCACTCTGGAACAGTCAGCAGCTTCCAAGGAATGACCCGCGCTCTCGCGAGC
 AAAGCTTCTGCCGCCAACAGACGAGAGCTCCCTCACTGCTGCAAGCCAGCTTGTGTGTGCTCAGCTTCTCCGCT
 ATCTCTGAGAGCTTGGGCACTTTCAGGCGCATGTATGACAAGATCTACTTTTTCTCAGCAGCACTGGCCAGAA
 TTTGATCTTTGAGAACCAATTGCTGTCCGCAATTGCCCGCATCTGCAAGGGCGATGAGGCTGGAGAGCGGGTG
 CTACAGCAGCGCTGGACCTCTCTCTCAAGGCCCCAGCTGTGTGCTCAAGCCCGCAGATGCTCTCCCTCTCACT
 GTGCTGAGAGTATCTTTCAGCTGTAGCGCCAGCCCGAGCACTGGCTGACACAGCTTTCTATGGGTTCTTCACT
 TCCAGTGTGACAGGAGATACAGAGAGCTCTGCCGCTGTGCTGTCTTCCAGTAAGGATGTGACAGAGATCTTCT
 AGCGGCGTCTACAGGAGGTGAACCGTGGAGACACAGCATGGTATCCAGTGACCCCGGTTGCCACACCCCGG
 CTGTGAGCGTGCTCATCCACAACTGTCGGCGGGAAGGAGATCAACTCATCTCTCGAGCTCCAGAGCCGCTGTGCT
 AACTTCTTCAGAGCACTTCTCTGATGACGGGCGAGTTCGAAGCGCATCTGCTGCTGTGACGCCACGCTCGT
 TACGACGCGCTGGCTGTACAGCCGCTCTCTGCGCTGTACACACACTTACGATGCTCTCTCTTGGCAGCTGGTGAC
 GGGCCGCTCCACAAAGCACTGAGCGTGGGCGCCCGGTTGCATCTTATGAGGAGCTCGAGATCTTCTCATCTGGGA
 CAGCCGCTGTGCAAGATTCTGCTCTGGACACCCAGGCGGGTGTCTGTCTCGGGCTCAACTCTGGGCGCTTGTCCAG
 GTGCCATTTGGCCAACTGAGCTGTACCCGAGCTGTGGGAATGCTGCTCTCGCGCGGACCCCTACTGTGCTGTT
 GCGGGCTCCAGTGTGCAAGCAGCTGACCTTACACGCTCACTGTGCCACAGCGGCTGGATTCAGAGACATCGAG
 GGAGCGACGCGCCAAAGCACTTTGACAGCGCTCTTGGTTGTGTGCTCCGCTTTTGTATACCAAGGGAAGAGCA
 TGTGAGGATGCTCAGTTCTCAGCCGCCCAACAGATGAACTCTTGGCTTCCGCGCTCTCTTCAACTCTGGCAGCCGA
 CTCTTGACTACGCAAGGGGCCCCGATCTGCTCTGCGCTCTGCTGACAGTGTACCTCTGGGACCTGTGCTGTG
 GTGGGCGCCCAACAGCTGTGGGGAGTTCCAGTGTGCTGTCTAGAGAGGGCTCTCCAGAGCTGGTATGAGCACTAC
 TGGCCAGAGGTGTGTGAGGACGGGGTGGCAGACAAACAGATGAGGTGTGCGAGTGTACCCGTCTATTATCAGCTA
 TCGGCTGTGAGTGTACCAAGCTGTGGCAGAGGCCAGTGGGGTGCAGACAGTCTCTAGGAAGGATCTTCTGTTG
 ATGTGACGCTTGTCTGCTGTGCGCGTGTCTTCCAGTTTATTTCTGTCTACCCGACCGGAACAGCATGAA
 GCTCTTCTTGAGCAGGAGGGAATGTGCAAGCTGTGCACCGCCAAAGACTCGCTTGTGGTGTGCCCTCTGAGACCGC
 CCATCTACCGCGCTAGGGGCCCCTAGACCCGCTGTATACCGAGGGTACCGTCCCTGTACAGACAGCCCCC
 GGGGCGGCGAGTGTCTCAGTATGAGCAGGAAGGCCACTCAGCATTCAGACAGCACTCTGTGAGGATTTCCCGATG
 TCGCCCGCGGCGCGGCTCGCCTTGGCTGGAGATCTGCTGATCTGTGAGTCTGAGAGCTACTCCAGAGACGT
 TGCCCTTGTCTTCAGGGGCTGTGAATTGCTCGGAGAGGTTCACTGAACTTCCTCTCGCTCTCTGCTGTGAAC
 AGCCGCTGTGTGCGGCGCTTGGGAGCTTGGAGCGACTTGCCTGTGCTGTCTGACTGATGAGTACGAGTCTTCA
 TACCCCAGACAGACCCAAACAGCTCGTGGCCCGAGAGTCTGTGCCCAATATGGGGGCGCTGCTAGTTGTGGTGA
 CAGTGTCTCTTATGTAACATGAGCCTTTGTTTAAAAAACATTCAAATGTGAACTAGATATGAGGGAAGAG
 ATAGATAGCGCATGACGACACACCGGCTGTCTCAGTTTCTATGGCTTCCAGGGGTGTGGGATGCTGCTCAAGTGTG
 TTGCTGTAGACAGATTTGGAACCTCTACCACTGGCTCTTCACTTCCATATCTTGTCTGCTGCTGCCACGGGTGCT
 CTTGCTCTACGTACGTAGATCAGGACAGCTTGGGCTGTGCTGCTTGTGCTTGCAGTTCAGCGAGGATGTATGTTG
 TTGCTGCGCTGCTCCACCACTCAGGACACCGGCGCTAGTTTGGCATCGGCGCTTACAGGCTCTGGGCTCT
 GGACCCAACTCTGGACCTTTCCAGCTGTATCAGGCTGTGAGCCAGCAGAGGACGAGGAGCTCGAGTCTAGGAGA
 TTTCTGTGTAACCTGTACGCTTTTCTCTCAGAAATCAGGGAAGAGACTGTCCGCTCTCTCTGCTGTGCTGTGA
 GAACCCGTTGGCCCCITCCACCATATTCACCTCTGCTTCATCTTTGAACTCAACACAGGAACATCACTGACCC
 CTGGTCTCTCCCGAGTCCCGAGTTCCACTCTCATCTCCCTTCTTCACTTAAGGATATCAACACTGCC
 AGCAACAGGGGCCGTGAATTTATGTGTTTATTATACATTTTTTAATAGATGCATCTTATGTCAATTTTAAATAA
 GCTCTGAAGAATTACTGTTTAAAAAATAAAAAA

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FIGURE 142

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSLAAPW GALPPRPPLLLLLLLLLLLQLPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLSRDGR TLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFS PMCTYINMENFTLARDEKGNVLE DGKGRCP
FDPNFKSTALVVDGELYTGTVSSSFQGN DPAISRSQSLRP TKTESSLNLWLDPAFVASAYIPE
SLGSLQGDDDKIYFFFSETGQEF EFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFFPNVLQDVFTLSPSPQDWRDTLFGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFLMDGQVR
SRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGR LHKAVSVGPRVHIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDC LLARDPYCAWSGSSCKHVS LYQP
QLATRPWIQDIEGASAKDLCSASSVVSPSFVPTGEKPCEQVQFQPNVTNTLACPLLSNLATR
LWLRNGAPVNASASCHVLPTGDLLLVGTQQLG EFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPIISTSRVSAPAGGKASWGADRSYWK EFLVMCTLFVLAVLLPVLFLLYRHRNSM
KVFLKQGE CASVHPKTCPVVLPPE TRPLNGLGPPSTPLDHRGYSLSDSPPGARVFTSEKR
PLSIQDSFVEVSPVCP RPRVRVLGSEIRDSV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGCGGCGGCGGCCGGCTACGAAGAGGACGGGGACAGGCCCGCTGCGAACC
 GACCCAGCCAGCCGGAGGACGCGGGGAGGGCGGACGGGAGCCCGGACTCGTCTGCCGCCGCCGCTGTCGCCCGTGC
 TGCCGCGCCCGCGTCCCGCGCGGAGCGGGAGGAGCGCGGCCACTCGCGCCGAGCGCGCGCTAGCGCGCGC
 CGGGCATGGTCCCTCTTTAAAGGCGCAGGCGCGCGCGCGGGCGGGTGTGCGGAACAAGCGCGCGCGCGGGG
 CTTGCGGCGCGCTCGGGGCGCGCATGGGCGCGCGGGCGCGCGCGCGCGCGTGGCCGGCGCGGCTCG
 CGCGCTAGGGCGGGCTGGCTTCGTGGCGGGGCGAGCGGGCTGAGGCGCGCGGAGCTGCGCGCGCGCGGCG
 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 TGCTCGGGCTCGTCTGGCTTCGTGCTGGCTCGCGGCTCGTCTGCCCGCGGCTCCGAGCTGAAGCGAGCGC
 GCCACGCGCGCGCGCGAGCCCCGAGGGCTGCCGCTCGGGGAGCGCGCGGCTCCGAGCGCGCGCGCGCGCG
 GCGATGCGCGCGGGCGCGAGCTCTGGCGCGCGGCTCGGACCCAGATGGCGCGCGCGCGCGAGCAACTTTCTCT
 TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCGTGGCGCGTACAGTAATGGTCCAAAGCAA
 TTCCTGGGAAAGTTCACTTCTCAAGTGAGGTTCTGACACATCTGTACCAATTCAGTAGTGCACTACGGG
 GTGTGGAGCACTCCTACCGCGCCAGAAAGTCCCTCATGATGCTCAAGTACATACACGACCACTACTTGGACA
 AGTATGAATGGTTATGAGAGCAGATGATGACGTGTACATCAAGGAGACCGCTCGGAGAACTCTCTGAGGAGTT
 TGAACAGCAGCGAGCCCTCTTTCTTGGCGAGACAGGCTGGGACACACGGAAGAAATGGGAAACTGGCCCTGG
 AGCCTGGTGAGAACTTCATGATGGGGGGGCTGGCGTGATCATGAGCGGGAGGTTGCTTCGGAGAATGGTGGCGC
 ACATTTGGCAAGTGTCTCGGGAGATGTACACCACTGAGGAGTGGGAGGTTGTCTCGGAGAGTTTTCG
 CAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCGAGCTTTTTATGAGAATACGAGCAGCAAAAAAGGGT
 ACATTAGAGATCTCCATAACGATATAATTCACCAAGCTATACATACACCCCAACAAACCAACCTTACGACT
 ACAGGCTCCACAGCTACATGCTGAGCGCAAGATATCCGAGCTCGGCCATCGCAACAATACAGCTGCACCGGAA
 TTGCTCTGATGAGCAATAACGACAACAGAAATTCATAAAGAGGACCTCCAGCTGGGAATCCCTCCCTCTTCFA
 TGAGGTTTACCGCCCGCGAGGAGAGATTCGGAATGGGAGTTTCTGACTTGAAATATCTTGTATTGGCGCAG
 TTGAGCGCCAGCCCTCGACGAGGAAATGGAATTCGCCCGCAGGGAAGCCTTGACGACATCTTGTATGAGCTCA
 TGGAGATGATCAATGCCAGCCGCAAGACAGAGGGCGCATCATTTGACTTCAAAGAGATCCAGTACGGCTACCGCC
 GGGTGAACCCATGTTGGGGCTGAGTACATCTTGACCTGCTGCTTCTGTAGAAAGCAGCAAAAGGGAAGAAAA
 TGACGGTCCCTGTGAGGAGACCGGATATTACAGCAGACTTTCAGCAAAATCCAGTTTCTGAGAGCATGAGGAG
 TGGATGACCAAGAGTTGGCCAGAGAATCAATCAGGAATCTGGATCTTGTCTTCTCAAACTCCCTGAAGA
 AGCTGTTCCCTTTCACTCCCTGGGTGGAAGAGTGAGCACAAAGAACCCAAAGATAAAAGATTAACATCATGA
 TTCTTTGTCTGGGCGTTTCGACATGTTTGTAGATTATGGGAACTTTGAGAAGCACTGCTTTATCCCAATGA
 AGAACCTCAAGCTCGTGGTCTGCTTTTCAATTCTGACTCCAACCTTGACAAGGCCAAACAGTTTGAAGCTGATGA
 GAGATTACCGCATTAAAGTACCTTAAAGCCGACATGCAATTTTGCCTGTGTCTGGAGAGTTTCAAGAGCCCTGG
 CCCTGGAAGTAGGATCTCCCTAGTTTAAACATGAATCTTGTCTTCTTCTGCGAGCTGACCTCGTGTTTTACTA
 CAGAATTCCTTCAGCGATGTGCGAGCAATACAGTTCTGGGCGCAACAAATATATTTTCCAACTATCTTCAGCCAGT
 ATGACCCAAAGATGTTTATAGTGGAAAGTTCACAGTGACAACCAATTTTGGCTTTTACTCAGAAAACCTGGCTCT
 GGAGAACCTATGGGTTTGGATCAGGTATTTATTAAGGAGATCTTGTCCAGTGGGTGGCTTTGATGTTTCCA
 TCCAAGCTGGGGGCTGGAGGATGTGACCTTTTCAACAGGTTTCCAGCGAGTTTGAAGAGCTTTAGGAGCG
 AGGAAGTAGAGTAGTCACCTCCACCTCTGTCTTTGTGATCCCAATCTTGACCCCAACAGCAAAAGATGT
 GCTTGGGGTCCAAGAGCTGACACTATGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAA
 GTTACAGTAAAGCAGCAATATAATGGCTCAGTGAGGACAGCTTAATGTCAAGTTTGTCTGGAAGAGCGTTT
 TAATTAATCTTAATTAATTTCAAAATTTTGTATGATCAGTTTGAAGTCCTGATACAGGATATATTTTAC
 AAGTGGTTTCTTCTACATAGACTCTTTAAGATTGAGCTTTTGAACAAGAGGTGATCAGTTGTTCCTTATGGA
 CACATCTTCTGTGTAACATGTATGACAGACCTGCTTAACITTGACTTGAATGTACCTGATGACAAACAACTT
 TTTAAAAAATGTTTCTTTTGAACCTTTGCTCAGTCTTATGGCAAGCGTGAACATCTCTGCAAGAT
 TATTGTACAAACACAGTCAACTCGGTAATGTTCTGTGTGATTGTAAACATCCACAGATTCTACCTTTGT
 GTTTGTTTCTTTTTTTACAACTGTTTAAAGCCATTTCATGTTCCAGTTGTAAGATAAAGAAATGTATATA
 CGTGTCTCATCATGTCTCAGAGAGCTTCCAGATTGATCTTCCCTCATGTGACTCTGCTCAGCATGCG
 CAGTAGGTTTCTTTGTTGTTTGTGTTTCTTTTGGAGCGGACTCTACTCTGTACCGAGCTGGAATG
 CAGTGGCGCAATCTTGGCTCACTTTAACTCCACTTCCCTGGTCAACCAATTCCTGCTTGGCTCCCGAGT
 AGCTGGGATTACAGCACACACCCAGCCAGTAGTTTGTATTTTGAAGATGAGCGGGTCCCACT
 CGAAGCCAGCTGGCCAGCTAGGTTTAAAGCAAGGGCGTGAAGAAGGACAGTAGGATGTGGCTGTCTCGT
 TGTGACTTCTTCTGCGCTAAATAGACTGGCATTAATTTCAAGAGGATTTGGCAATTTCTCTCTTGACCTT
 CTCTTTAAGGGTAAATATTAATGTTTAGAATGACAAAGATGAATATTTACATAAATCTGATGTACACAGT
 GAAACATACACACATACCCCTAATCAAAAGTTGGGGAATAATGATTGGTTTGTCTTCTTACCTCTGCTG
 TGTATGTAGTGGTGGAGATGGTTTTCATCTTTTCAATGTTTGTGTTTGTGTTGTTGTTGTTGTTGTTGTTG
 TTTATTTAATATCTGTTTTCAGAGCTGCCATTTCTGAGTACCTGTTAGTTAGTATTATTGATGTACCG
 GAGTGTGTTTGTGTTTATTTTGCAGTAAACCGATCCCAAGATTTCCTTTGGAAACGCTTTTTCCTCCCTC

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FIGURE 143B

TTAATTTTATATTCCTTACTGTTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTGGG
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTTGTT
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACAGTCATTGGAGGGCTGCGTATTTGTAAATAG
CCTGATGCTCATTGGAAAAATAAACAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGTCTCATT
ATTCCTGTTTtagctgaagaattgtattacatttggagagtaaaaaacttaaacacgaaaaaa

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FIGURE 144

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAAGRRRAWLSVLLGLVLGVFLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMATAQKYLQTRAAAYRTWSKTIPGKVQFFSSEG
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFMRADDDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSRVLRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCWVSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQPRQEE
ILEWEFLTGKYLVSADVGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNPYGAEYILDLLLLYKHKHGKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFSLNSLKKLVFPQLPGSKSEHKPEPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVLVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT
QKTGFWRNYGFGITCIYKGDIVRVGGFDVSIQGWGLEDVDLFNKVVQAGLKTFRSQEVGVVH
VHHVPVFCDPNLDPKQYKMLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA
```

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACCGTTGCTGGGTGTCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC
 TTTCGGCCTTGAGGTTCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT
 ACGGACGACGCCT**ATGA**AGCCCTTAGTCCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGCTG
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA
 CAAGTTTGTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATC
 TAACCTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA
 CACATGGAGACGCTTCAACTGAGAATGATGTTTAAACCAATCCTATCAGTGAAGAACTACA
 ACTTTCCTTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC
 ATTCTGGTCGATCAAACCAAACATGTTTCCATTGTTTTCATGCAGAGGAACCTTATATTG
 AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG
 TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTAC
 CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT
 CAGGTGAAACTGCGATAGAAAAACCCGAAGAGTTTGGAAAGCACCCAGAGAGTTGGAATAAT
 GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGA
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAACGAAGCC
 TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCAGTTATTGCCA
 GTAGGACGAACAAGTAATAAAATTGATGACATCGAACTGTTATTAACATGCTGTGTAATTC
 TAGATCTAAACTCTATGAATATTTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAG
 CTGTACAGTATTCAATACATTAATAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
 AAAGTTTAT**TAA**ACAATAATATAAAAAATTTTAAACCTACTTGATATTCCATAACAAAGCTGA
 TTTAAGCAAACCTGCATTTTTTCACAGGAGAAATAATCATATTTCGTAATTTCAAAGTTGTAT
 AAAAAATTTTCTATTGTAGTCAAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACA
 ATTTTCATATGCACTAAAAACCTAATTTAAATAAAATTTTGGTTCAGGAAAAA

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FIGURE 146

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864

><subunit 1 of 1, 350 aa, 1 stop .

><MW: 39003, pI: 5.59, NX(S/T): 1

MKPLVLLVALLLPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVSPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTFTPTGGFTPEIGKKKHTESTPFWSI
KPNNVSIVLHAEPEYIENEEPEPEPEPAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK
STGIEISTESEDVLPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSQVQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPPMEMREKAATVFNTLKNMCRSRRVTALLKVY

Signal peptide:

amino acids 1-19

FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGACCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG
ACCTCCAAATCATCCATCCACCCCTGCTGTCACTCTGTTTTCATAGTGTGAGATCAACCCACA
GGAATATCCATGGCCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGACA
GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCTTGGTGGGGGAGGACGCCGTGTTCT
CCTGCTCCCTCTTTTCTGAGACCAAGTGCAGAGGCTATGGAAGTCGGGTCTTTCAGGAATCAG
TTCCATGCTGTGGTCCACTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA
GTATCGAGGGAGAAGTGTGTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGC
TAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTTCAGTTCCAGATTATAC
GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCTCTCATTTCCAT
CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCTCCACGC
CCACGCCAAGTGGAAAGGTCCACAAGGACAGGATTGTCTTCAGACTCCAGAGCAAAATGCA
GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAAATGCTGGGAGCAT
ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG
AGACGTTTTTCCAGCCCTCACCTTGGCGCTGGCTTCTATTTTACTCGGGTACTCTGTGGT
GCCCTGTGTGGTGTGTCTATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAAATCCA
GGCGGAAGTCACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGGAAAAACAG
CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA
ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAA
GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC
AAAATGTAGGTTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGGAAGAACAATGTG
ACTTTGTCTCCCAAGTAATGGGTATTGGGTCTCAGACTGACACAGACATTTGTATTTCAC
ATTCAATCCCCATTTTATCAGCCTCCCCCCCCAGCACCCTCCTACACAGTAGGGGTCTTCC
TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC
CTGCTGACATGTCAAGTTTGAAGGCTTGTGAGACCTATATCCAGCATGCGATGTATAGCAGA
GGAAAAGGGGACTCCCATATTCATATGTCAGATGTCTTGGGGATGAGACAGAGAAGACCTG
CTTAAGGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGC
CCCAGCTTCTCTCCGGAGCCTGCGCACAGAGAGTACGCCCCCCTCATCTCCTTTAGGGAGC
TGAGGTCTTCTGCCCTGAGCCCTGCAGCAGCGGCAGTCAACGCTTCCAGATGAGGGGGGAT
TGGCCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA
CATTAGGTTTAGTTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCAAACTCC
CAGGCTCCTCATTTGCTAGTCACGGACAGTGATTCTTGCTCACAGGTGAAGATTAAGAGA
CAACGAATGTGAATCATGCTTGACGTTTGAGGGCAGAGTTTGTGATGATGTGTTTTTA
TATTATACATTTTCCACCATAACTCTGTTTGCTTATTCACATTAATTTACTTTTCTCTCA
TACCAAATCACCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAAATAAGAG
GAGGTAGGATTTTTCACTGATTCTATAAGCCAGCATTACCTGATACCAAACAGGCAAG
AAAACAGAAGAAGAGGAAGGAAAACTACAGGTCCATATCCCTCATTAACACAGACACAAAA
TTCTAAATAAAATTTTAAACAAATTAACATAAACAATATTTAAAGATGATATATACTACT
CAGTGTGGTTTGTCCACAAATGCAGAGTTGGTTTTAATATTTAAATATCAACCAGTGTAAAT
CAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAA

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FIGURE 148

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQVQTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIVQENAGSILCSIHAEQSHEVESKVLIGETTFQPPWRLASILLGLLGCALC
GVVMGMIIIVFFKSKGKIQAELEDWRRKHGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTTCATTGCTGTTGGCA**ATG**ATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAGAGTTTTGTTGGGAACCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTCT
 CTGGCAGTGTGCATTGGACTCACTGTTTCATTATGTGAGATATAATCAAAGAAGACCTACAA
 TTACTATAGCACATTGTCATTTACAACGACAACTATATGCTGAGTTTGGCAGAGAGGCTT
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA
 TCTCCATTAAGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG
 AGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG
 ATAAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA
 GATCCTCACTCAGTTAAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACACGAAGAAGTAAACTCTAGGTGAGAGTCTCAGGATCGTTGGTGGGACAG
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTACAACATATAA
 GAACCTGCCAGATGGACTGCTTCCTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG
 GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCT
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA
 TGCATCCTATGAGTTTCAACAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA
 ATGATGGTTACAGTCAAATCATCTTCGACAAGCACAGGTGACTCTCATAGAGCTACAAC
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT
 AGAAGGAAAAACAGATGCATGCCAGGGTGAAGTCTGGAGGACCAGTGGTTAGTTCAGATGCTA
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGAGATGAATGTGCGAAACCAACAAG
 CTTGGTGTTTATACTAGAGTTACGGCCTTGCGGACTGGATTACTTCAAAAACCTGGTATCT**TA**
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTGGGTGTGGAGGCCATT
 TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGGATTTGACTGATCTCAATAAAC
 TGTTTGCTTGATGCATGTATTTCTTCCAGCTCTGTTCCAGCTGAAGCATGCTGCTGCTCTG
 CCAGATCAACTCTGTCTCTGTGAGCAATAGTTGAAACCTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCAATTTGTTCTCTAGAAGTTTTGTGCAATTTTGAC
 TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTC
 AGCTCCTCTCATTTCAAGCAATATCCATTTTCAAGGTGCAGAACAGGAGTGAAAGAAAATA
 TAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT
 GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAGACAGCAGAAATACCAATC
 ACTTCATCATTTAGGAAGTATGGGAACAAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA
 TCCTTATTTTCATTTCCAAACAACTACTATGATAAATGTGAAGAAAGATTCTGTTTTTTTGTG
 ACCTATAATAATTATACAAACTTCATGCAATGTACTTGTTCTAAGCAAATTAAGCAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

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FIGURE 150

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYNSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLEEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCTRRSKTL
GQSLRIVGGTEVEEGEWPQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVYPYTNVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWIYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI
```

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

GTCGAAGGTTATAAAAAGCTTCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA
 CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTGAGCTGGTGGATTCCCG
 CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
 CGTGACCTTCTTGGTTCACAGAGCTCAGCCCTTGGCCCTCAAGACTTTGAAGAAGAGGAGG
 CAGATGAGACTGAGACGGCGTGGCCGCCCTTGGCCGCTGTCCCTGCGACTACGACCACTGC
 CGACACCTGCAAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCGGCTGCCTGTGCCC
 AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG
 CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCGGTCTCTCACTACTGG
 CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGGCCCCGCTGAACGCTACGGTCCG
 CAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTATGTCTGTTTGGCTAGTGGCCGCTA
 ACGAGGCCGGGGCAAGCCGCGTGGCCCAAGGCTGGAGGAGAGGGCTCGAGGGGGCCGACATC
 CCTGCCTTCGGGCTTGCAGCCGCCCTTGGGTGCGGCCCAACCCCCGCACTCTGGTCCACGC
 GGCCGTGCGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
 GCCTGCGCGATCGCTGGGGCTGCCCGCGCCGAGCCGCCGCCGAGCCGCAGGGGGCGCTC**TGA**
 AAGGGGCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCG
 GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG
 GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT
 GGCGCTTTGTTTCTTGGCTGAGGTCTGGGAAGGAATAGAAAGGGCCCCCAATTTTCTTTTA
 AGCGGCCAGATAATAAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

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FIGURE 152

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQPLAPQDFFFFFFEADETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLCPLGSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLDGSEA
AQKGPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRVPOAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVAHAVGVGTALALLSCAALVWHFCLRDWRGCPRRAAARAAGAL
```

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC
 CTGCCCCGATGAGCCCCCGCGTGCCTCCCGACTATCCCCAGGCGGGCGTGGGGCACC
 CCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGG
 TTCTCCCTTACGGGGCTCACATGGCCAGAGAAGATTCCGTGAAGTGTCTGCCGTGCCTGCT
 CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCATCAGTGTGTGGCAGTTTTCTGCTTGG
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC
 ATTTTGACTTACTTTCTGTGGTTCATCCGGTCATGATTGCTGTTTGGCTGTTTCTTATCAT
 TGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACT
 TTGGAAGTTTGCTTGTCACTTTCTGTGTAGAACTGGCTTTGGCGCTTTGGACATATGAACAG
 GAACCTATGGTTCCAGTACAATGGTCAGATATGGTCACCTTGAAAGCCAGGATGACAAATTA
 TGGATTACCTAGATATCGTGGCTTACTCATGCTTGGAAATTTTTTTCAGAGAGAGTTTAAGT
 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAATGACAGAGATGGACTGGCCCCAGAT
 TCCTGCTGTGTTAGAGAATTCACAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGA
 CCTTTATCAAGAGGGTTTGGGAAGAAATGTATTCCTTTTGAGAGGAACCAACCACTGC
 AAGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAATGATGTC
 CTTGAAGAATGACAACCTCTCAGCACCTGTCTATGTCCTCAGTAGAACTGTTGAAACCAAGCC
 TGTCAAGAATCTTTGAACACACATCCATGGCAACAGCTTTAATACACACTTTGAGATGGAG
 GAGTTAT~~TA~~AGAAAGAAATGTCACAGAAGAAACCAACCACTGTTTTATTGGACTTGTGAATT
 TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAATGTTGCCATAAAATAACA
 CCTAAGCATATACTATTCTATGCTTTAAAAATGAGGATGAAAAAGTTTCATGTCTAAGTCAC
 CACCTGGACAATAATTGATGCCCTTAAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTT
 CGCATCCATGCAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTACTT
 CTACCAACTAGTATATAAAGTACTAATTAATGCTAACATAGGAAGTTAGAAAATACTAATA
 ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATATATATCAGAAAACCTTC
 AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCCTTAAAA
 GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGATATATAAGTCTGTGTAA
 TCTGTATAATTCAGTCGATTTTCACTTCTGATAATGTTAAGAATAACCATATGAAAAGGAAA
 ATTTGTCCTGTATAGCATCATATTTTTAGCCTTTCTGTAAATAAAGCTTTACTATTCTGT
 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAATTA
 CCAGTGTGATACATAGGAATCATTTATTCAGAAATGATGCTGGCTTTAGGAAGTATTAATA
 GAAATTTGCACATAACTTAGTTGATTGAGAAAGGACTTGTATGCTGTTTTCTCCCAATG
 AAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCTCTCCAAACAGAA
 GCAATAGTCTCCAAGTCAATATAAATCTACAGAAAATAGTGTTCTTTTTCTCCAGAAAAT
 GCTTGTGAGAATCATTAACATATGTGACAATTTAGAGATTCTTTGTTTTTACTGATTAT
 ATATAGTGTGGCAAAATTACACAGATTATTAATTTTTTACAAAGATAGTATATTTATTT
 GAAATGGGAAAAGTGCATTTTACTGTATTTTGTGATTTTGTGTTATTTCTCAGAAATATGGAA
 AGAAATTAATATGTGCAATAAATATTTTCTAGAGAGTAA

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FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAE TRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWVTYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEDWPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCC
 TGCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
 ACCGGGAGGATCAGAGAGCCAGC**ATG**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGC
 CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT
 CCCCATCATATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTGTCTCATCAAGG
 TGATCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAG
 CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT
 CCCCAGGGCCTGCAGTGCGAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
 ACTCGGCCACAGGGAAC**TGG**TTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG
 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGA
 TGTGTGTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTC
 TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCCTGTGGGAAGAGCCTGAAGACCCCCCGT
 GTGGTGGGTGGGGAGGAGCCCTCTGTGGATTCTTGCCCTTGGCAGGTGAGCATCCAGTACGA
 CAAACAGCAGCTGTGTGGAGGGAGCATCCTGGACCCCACTGGGTCTCACGGCAGCCCACT
 GCTTCAGGAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGC
 AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCACCCCATGTACCCCAA
 AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCTCACTCACTTCTCAGGCACAGTCAGGC
 CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA
 TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGCTAGTCCA
 GGTCAATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGA
 TGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCC
 CTGATGTACCAATCTGACACAGTGCGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG
 GGGCCCCAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
 TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCTGTG
 CCCTGCCCACTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCTTGGGTACACCC
 CTCTGCCACAGCCTCAGCATTTCTTGGAGCAGCAAAGGGCTCAATTCTGTAAAGAGACCC
 TCGCAGCCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC
 AGCATCCCAGGGAGAGACACAGCCCACTGAAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA
 GGAACCTTCCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCCAGATCACTGTGGG
 CTGGAGAGGAGAAGGAAGGGTCTGCGCCAGCCCTGTCCGTCTTCACCCATCCCCAAGCCTA
 CTAGAGCAAGAAACCAGTTGTAATATAAAATGCACATGCCCCACTGTTGGTATGACTACCGTT
 ACCTACTGTTGTCAATTGTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT
 CTGGCAAAAAAAAAA

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FIGURE 156

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPPIIIALLSLASIIIVVLIKVILDKYYF
LCGQPLHFI PRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAEACRQMGYSRAVEIGPDQDL DVVEITENSQELRMNRSSGPCLSGSLVSL
HCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVCSSILDPHWLTAACHFRKHTDV
FNWKVRAGSDKLGSPSLAVAKIIIEFNPMYPKDN DIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMM CAGIPE
GGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
```

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAAGGGAGGGAAACGACAGCGGCATCCCCAGGCTCCAG
 AGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCCCTGGACCCCTGGAGCCCTCTGGGCC
 TTTTCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACAGCCGCGGGGGAGGGGGCAGGGGCCCATGCCCA
 GGGTCAGATACTATGACAGGGGATGAACGTAGGGCAGCTTAGCTTCTTCCACCAGAAAGGGCCCTCAGGATTTTGACA
 CTCTGCTCTAGTGGTGGTGAATGATCTCTACGTGGGGCTCGAAGAGCCATCTTGCCCTCTGGATATCCAGG
 ATCCAGGGGTCGCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCCTTTA
 AGAAGAAGAGCAATGAGACAGCTGTTCAACTTCATCCGTGCTCGTTTCTTACAATGTCAACCATCTCTACA
 CCTGCGGCACCTTCGCTTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGATTCTACCTGTTGCCCATCTCGG
 AGGACAAGGTCATGGAGGAAAGCCCAAGCCCTTTGACCCGCTCAAGCATACGGCTGTGCTTGGTGAGT
 GGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCATCCTGATGCGCACACTGGGATCCCAGC
 CTGCTCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCTCCTTTGTGGCAGCCATCCCTTCGACCC
 AGGTCGTCTACTTCTTCTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG
 CTAGAGTCTGCAAGAATGACGTGGCGGCGAAAGCTGTGCGAAGAAAGTGACACCTCTCTGAAGGCCCTGACCT
 TGCTCTGCACCCAGCCGGGCGAGCTGCCCTCAACGTCAATCCGCCACGCGGTCTGCTCCCGCCGATTCTCCCA
 CAGCTCCCCACATCTAGCAGTCTTCACTCCCAAGTGGCAGGTTGGCGGGACAGGAGCTCTCGGGTTTGTGCT
 TCTCTCTCTTGACATTTGAACGTGCTTTAAAGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTA
 CTTATAGGGGCCCTGAGAGCAACCCCGCCAGGCAAGTTGCTCAGTGGCCCTCCTCTGATAAGGCCCTGACCT
 TCATGAAGGACATTTCTGTATGGATGAGCAAGTGGTGGGACGCCCTGCTGGTGAATCTGGCGTGGATATA
 CACGGCTTGCAAGTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTATGTACTGGGAACCCACACAG
 GGTGCTCCAAAGGCTGTGGTAAGTGGGACAGCAGTGCTCATCTGTTGAAGAGATTCAGCTGTTCCCTGACC
 CTGAACCTCTTGCAGCACTCGAGCTGGCCCCACCCAGGTCAGTGTTGTAGGCTTCTCAGAGAGTGCTGGA
 GGGTGGCCCGAGCAACTGTAGTGTCTATGAGAGCTGTGTGACTGTGCTCTTGGCCGGGACCCCATCTGCTCT
 GGGACCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCAACCTGAATCCTGGAAGCAGGACATGGAGCGGG
 GGAACCCAGAGTGGGCATGTGCCAGTGCCCATGAGCAGGAGCCTTGGCCCTCAGAGCGCCCGCAAAATCATT
 AAGAGTCTGTGGCTGTCCCAACTCCATCTTGAGCTGCCCTGCCCCACCTGTGAGCCTTGCCCTCTTATTATT
 GGAGTCTAGGCCACAGCAGATCCCAAGACCTCTTCCACTGTCTACAATGGCTCCCTCTTGTGATAGTGAAG
 ATGGAGTTGGGGTCTCTACAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGG
 ACAGCCAGGACCAAGCCTGGCCCTGGATCCTGAATGGCAGGCATCCCGGGGAGCATGTGAAGGTCCCGTTGA
 CAGGGTCAGTGTTGGGGCCGCCCTGGCTGCCAGCAGTCTTACTGGCCCACTTTGTCACTGTCACTGTCTCT
 TTGCCCTAGTCTTTCAGGAGCCCTCATCATCTCTGTCGCTGCCCTCCCCATTGAGAGCATCCGGCTCGGGGCAAG
 TTCAGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAG
 AATGCAAGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCAGCTGAGGTAGCTTAAACTCTAGGCA
 CAGGCCGGGGCTCGGTCAGGACCTGGCCATGCTGGCTGGGGGGCCCAAGCAGCCCTGACTAGGATGACAG
 CAGCACAAAAGACCACTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGACTCATGATGACACTCAGCAGGGTG
 ATGCACAGCAGTCTGCCCTCCCTATGGGACTCCCTTCTACCAAGCAGATGAGCTCTTAACAGGGTGGGGCTAC
 CCCAGACCTGCTCCTACATGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCCT
 CAGAAACACAGTGTTCAGAGACCCATAAAAAACCTGCCTGTCCAGGACCCATGGTAATGAACACCAAAATC
 TAAACAATCATATGCTAATATGCCACTCTGGAACCTCCACTCTGAAGCTGGCGCTTGGACACCAACCACTCCCT
 TCTCCAGGGTCATGCAAGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCCTGACTCCAGGAAGTC
 TTTCTGAAGTCTGACCACCTTCTTCTGTCTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAAATGG
 CAGGGGTAATCTGAGCCTTCTCACTCCTTACCTTAGCTGACCCCTTCACTCTCCCTCCCTTTCTCTTGT
 TTTGGGATTCAGAAAAGCTGCTGTGACAGACTGTTATTTTTATTAAAAATATAAGGCTTAAAAAA

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FIGURE 158

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop .
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGMPRVRYYAGDERRALSFFHQKGLQ
DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMI PWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGMTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDSFVAAIPSTQVVVFFFE
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQVVGGRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGSLLHKAVVSGDSSAHLVEEIQLPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESTRCTCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAPVEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFALVLSGALIIIVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVADADNNCLGTEVA
```

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAG
 TGAG**ATG**GCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCTTCTCCCTGGGGTCTCTGCTC
 TCAGAGGCTGCCAAAATCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
 CCGGTTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCCACATGCTTAAACCACAAAAGAG
 GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA
 CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGGAAGAACTTTAGG
 TGGCAGAGGAAAAATTTGAAACATTATTAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC
 ATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAAATGAGAACTTCGCATGGTGATA
 GTTGAAACTTTTGACTACTGTCTTTCTTGATTGCTGAGAAGCTTGGGAAGCCATTGTGGC
 CATTCTTTCCACTTCATTCCGGCTCTTTGGAATTTGGGCTACCAATCCCTTGTCTTATGTTCT
 CAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTCTG
 ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA
 GGAACATTTACAGAAGGCTCTAGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT
 GGTTCATTAACTCTGACTTTGCCCTTTGATTTTGTCTGACCTCTGCTTCCCAACACTGTTTAT
 GTTGAGGCTTGATGGA AAAACCTATTAAACAGTACCACAAGACTTGGGAACCTTCATTGC
 CAAGTTTGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACTGTCCAGA
 ATCCGGAATCTTCAAGGAGATGAACAATGCCCTTGTCTACCTACCCCAAGGGGTGATATGG
 AAGTGTCAAGTTCTCATTTGGCCCAAAGATGTCCACCTGGCTGCAAAATGTGAAAATTTGGA
 CTGGCTTCCCTCAGAGTGACCTCCTGGCTCACCAAGCATCCGTCTGTTTGTCAACCCACGGCG
 GGCAGAAATAGCATAATGGAGGCCATCCAGCATGTTGTGCCATGGTGGGGATCCCTCTCTTT
 GGAGACCAAGCTGAAACATGGTCCGAGTGAAGCCAAAAGTTTGGTGTTTCTATTCAAGT
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCTGGAAGACAAAGAT
 ACAAGTCCGCGGAGTGCTGCCAGTGTATCCTGCGCTCCCAACCGCTCAGCCCCACACAG
 CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCAGCACCTCAAGCCCTA
 TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGC
 TCACTCTGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCT
 GGGGCCAGAAAGGTGAAGGAGAC**TAA**GGCCAGGTGCAGCTTGGCGGGGCTGTTTTGGTGG
 GCGATGTCAACATTTCTAGGGAGCTTCCCACTAGTTCTGCGCAGCCCCATTTCTCTAGTCTCTC
 TAGTTATCTCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAATCATCTTTCCACTTGC
 TAATTTTGTACAAATTCTATCTTACTAGCTCCTGCTGCTAGCAGAAATCTTTCCAGTCTCT
 CTGTCTCTCTTTGTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG
 GACCATGACCTCAGATTTCCAGECTTAAATCCACCTTCTCTCATGGCCTCTCCGAA
 TCACACCTTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCT
 TACTATCTATCATGGAATTAACATCCAAGAAAGACACCTTGCATATCTTTCAGTTTCTGTGTT
 GTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAAGGC
 CGGACACAGGCTCACAGGTCTCCACATTTGGGTCCCTGTCTCTGGTGGCCACAGTGAGCTCTC
 TCTTGGCTGACAGGCTAGGAGACTGTAGGTTTCCAGATTCTCTGAAAAATAAAAGTTTACA
 CGGTATCTCTCCCAACCTCACTAA

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FIGURE 160

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGGKPFVAILSTSFGSLEFGLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHETEGSRPVLSHLLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP EIFKEMNNAFAHLPQGVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPsirLfvTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPWHEQYLFDFVFVLLGLTLGTLWLCCGKLLGMAVWWLRGARKVKET

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
 GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACATACCATGTT
 TCCATFCCCCCAGGTCAGCCCTCAGTGCTGCCATCCAGCAGGCTACCTGAAGCTCT
 GGCTGCAGCCCTCCGCTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCA
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTCAGCGAGCCTAGAGAGGGC
 AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAACAGAAGAGGGGCAGA
 AGACCGGGGCATTGTGGGTTGCAGAGCCCTCAGCCATGTTGGGAGCCAAGCCACACTGGC
 TACCAGGTCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC
 GGGTGGGCCCAGGAGGGGGTCCAGAGCCCGTCTCTGGAGGGGGAGTGCCTGGTGGTCTGTGA
 GCCTGGCCGAGCTGCTGCAGGGGGGCCCGGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC
 GAGTGGCATTGCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC
 ACCAGTGGGGCCATCTACTTCGACCAGGTCTTGGTGAACGAGGGCGGTGGCTTTGACCGGGC
 CTCTGGCTCCTTCGTAGCCCTGTCCGGGGTGCTACAGCTTCCGGTTCATGTGGTGAAGG
 TGTACAACCGCCAACTGTCCAGGTGAGCCTGATGCTGAACAGTGGCCTGTCTATCTCAGCC
 TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACAGCTCTGTGCTACTGCGCTTGGAA
 CCCTGGGACCCGAGTGTCTCTGCGCTGCGTGGGGGAATCTACTGGGTGGTGGAAATACT
 CAAGTTTCTCTGGCTTCTCTCATCTTCCCTCTCTGAGGACCCCAAGTCTTTCAAGCACAAAGAT
 CCAGCCCCGTGACAACTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG
 ACTCCTCTGGCTCCTATCCCACTCTTTGCTAGGGACCCCTGTGCCAAACACCCCAAGTTTAA
 GAGAAGAGTAGAGTGTGGCATCTCCAGACAGGCCCTTCCACCCACCCACCCCCAGTTTACC
 CTCCCAGCCACCTGCTGCATCTGTTCCTGCGCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCA
 AGAAGGAAGATCTGCACTACTTTGCGGCTCTGCTCCTCCGGTTCCCCCACCCAGCTTCTCT
 GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGCCAG
 ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATC
 TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGCTGGGAGGCTCAGCCAC
 AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTG
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
 GGCTGCTCCTTCTATGCTGGATCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
 GGTGAGTGTGTTTGTCTGTGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
 ACCATTGGAACATCGATAACCATGCATCCTCTTGTCTGGCCACCTCCTGAAACTGCTCCAC
 CTTTGAAGTTTGAACCTTAGTCCCTCCACACTCTGACTGCTGCTCCTTCCCTCCGAGCTCTC
 TCACGTAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTCTCCTGAT
 CTGTGCTGCTTATTCTCCTCCTTAGGCTTCCATTACCTGGGATTCATGATTCACTTCTT
 CAGACCCTCTCCTGCCAGTATGCTAAACCTCCTCTCTCTTCTTATCCGCTGTCCCAT
 GGCCAGCTTGGATGAATCTATCAATAAAACAAGTAGAGAAATGGTGGTCACTGAGACACTAT
 AGAATTACTAAGGAGGAAGATGCCTCTGGAGTTGGATCGGCTTACAGGTACAAGTAGGTA
 TGTTGCAGAGGAAAATAAATATCAAACCTGTATACTAAATTAATAA

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FIGURE 162

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVLLLEGECIVVCEPGRAAAGGP
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGLIFPL

Signal peptide:

amino acids 1-32

[illegible]

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FIGURE 164

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIADVLYFTWLVFDWNTPKKGGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMSSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM
PGKNAVTLNRNKGFKLALRHGADLVPIYSFGENEVYKQVIFEEGSGRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYEALVKLFDK
HKTKFGLPETEVLEVN
```

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

GGCGCGCGGATGGGGGCGGGGCGCGGCGCGCACTCGTGAGGCCCCAGCAGCAGGGCCGGGCGGGCCGA
GGCGCGGAGGAGCGCGGCGCGCCAGCAGCGGGGCGCGGAGGAGCAGCGCGGGGACGCCCGCGCAGCAGCAGGTGGCG
CGCGGCTGCTGACGCTTGTCCAGCCGGAAGCCCTGAGGGCAGCTGTTCCTACCTGTCTGCACTTGTGCCTTGA
CGCGTGTCTTAGCAGGGGCGCTGCACCGCGCTCTGACAGCAGCAATGGCGCTGTGGCTTCTCTGAAGAACGA
GTTCTGTGTGCACCTGCTGGTGGCTTTGTCTTCTGTGTGAGTGGTCTGGTCATCAACTTCGTCCAGCTGTGCAC
GCTGGCGCTGTGGCGGTGACGAGCAGCTTACCGCGCGCTCAACTGCCGCTCGCTACTCACTCTGGAGCCA
ACTGGTTCATGCTGTGGATGTTGTTCTGCACGAGATGTACACTGTTACGAGCAGCGCAGCTAGAGCGCTT
TGGGAGGAGCAGCAGCATCATCTCATCCCAACTTCAGATGCAGTCTTCTGTGGGTGGACCATGTGTGA
CGCGTTCGAGTGTCTGGGAGCTCAAGGTCTCGCTAAGAAAGACAGCTGCTTACGTGCGCCCTCATCGGCTGAG
GTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGAAGTGGGAGGAGGACCGGACACCGTGGTCGAAGGGCTGAG
CGCGCTGTGCGACTACCCGAGTACATGTGGTTTCTCTGTACTGCGAGGGGAGCGGCTTCACGAGACCAAGCA
CCGCGTTAGCATGTGAGGTGGCGGCTGCTAAGGGGCTTCTGTCTCAAGTACACCTGCTGCCCGGACCAAGG
CTTCACCAACCGAGTCAAGTGCCTCGCGGAGCAGTGCAGCTGTCTATGATGTAACTCTCAGGAGAAA
CAAGAACCCGTCCTGTGGGATCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTGAGGAGATTCTCT
GGAAGACATCCCGCTGGATGAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACAGGAGAAAGGACGCGCTCCA
GGAGATATATATACAGAAGGGCATGTTTCAGGGGAGCAGTTAAGCCTGCCCGAGGGCGTGGACCTCCTGAA
CTTCCGTGCTCGACCCACCATCTCTCTGCTCCCTCTTCAAGTTTGTCTGGGCGTCTTGGCAGCGGATACG
TCTCTGATCTGACTTCTTGGGGTTTGGGAGCAGCTCTCTTGTGAGTTGCGAGATGATGAGGAACTCCGT
TGAACCTGGGAGGTGGAGATTGCAGTGGAGCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT
CAGTCTCAAAAAAAAAAAAAAAAACAAAAAAAAAACCCAGAAATTCGGAGTTGAACTGTGTAGTTACTGACATGAAA
ATTCACTAGAGGCTGAACAGCAGATTGTGAGCAGGCAAAAAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT
TTTACGGCTAATGAAAAAGAAATGAAGAAAATTAAAGCTCAGAGACCAATGGTGACCGCTCACACAAATCAA
CATATGCATGATGAGAGTCCCAAGAGAGAGAGAAAGGCTCAGAAAGAAATGGCCACAGCTGATGAAAAACA
GTAACCTACCCACTCAGGAAGCTCAGTGAATCCCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTTCA
AATCAAAGTGTCAAATGACAAAGACTTGAAGACAGCAAGAGATGAGCACTTATCTTTGTTCAAAGGATCTTTG
ATCAGATTAAACAGCTCATTTCTCTCAGAAATCATGGGAGCAGGATAGTGGGATGAACACTGTTGAAGTTTCA
AACCTTCAACTGTAATTATGGACATTGTAGCTTTAGATGGTCTGACCTCTTGTCTTCAGGAGACATTTGAA
ATTTAATCCCTAATAACAATTAGTCAAGCTTCTTGACCTGTAGGAAGGCCTGTCTTTAGGCCGGGCACAGTGGC
TTACACTGTAAATCCAGCACTTGGGAGGCGCAGACGGTGGATCATTTGGGTCAGGCTGATCTCAAACCTCT
GAGTTCAAGTGATCTGCCCGCTCAGCCTCCCAAGTGTGTGATTGACGGCTGAGGCACCTGCGCTGGCCGA
ATTTCTTTTAAAGCTGAATGATGGGGGCGAGCAGATGGCTCAGCGCTGTGATCCCAAGTAGTATGGATGTA
ACAATGACCAACAGCTCGCTGGCTAATTTTGTATTTTATGATAGACAGCTGTAGCAGGCTGGTCTCGATCTCT
GACCTCAAGTGACCACCTGCCCTCAGCTCCCAAAGTACTGGGATTACAGGCGTGAGCAGCTGTGCCTGGCCTTGA
GCATCTGTGATGTGCTTATTTGGCCATTTGTATATCTTCTATCTTCTTGGGGAAGTGTGCTTCAAGTCCCTTG
CCTTTTTAAATTTTATTTATTTATTTATTTATTTTGTAGACAGGCTTGTGCTGTTGGCCAGGCTGGAGTA
CAGTGCGACAGCTGTGGCTCACTCAGCGCTCAGCTCTGGGTCAGTATCTCCCACTCAGCTCCCTCTGT
AGCTGATTTTTTTGTATTTTGTATTTTGTAGCTGTAGTTTTTGTATTTTTTGTGGAGACAGCATTTTACCATGA
TGCCCGAGGCTGGTCTGAACTCCTGAGCTCAAGTGATCTGCCGTCTCAGCCTCCCAAAGTGTGGGATTACAGA
GTAGGACCTGACTCCTGGCAACTCCCAAAATCAACACACAGCAAAAAACCACTGATTCAAATGGGCA
GAGGGGCGGGTGTGGCCCCAACTACAGGGAGACTGAAGTGGAGGATCGCTTGGGCATGAGAAGCTCAGGCTG
CAGTGAAGTCAGGTGTGTCGCACTGCATTCAGCGCTGACAGCAGGAGTGAAGCAGCTCTC

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FIGURE 166

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop .
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFFVVSGLVINQVQLCTLALWPVSKQLYRRLNCRSLWSQLV
MLELWWSCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKRR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN
FLSWATILLSPLFSFVLGVFASGSPLLILTFLGVGAASFGVRRLLIGESLEPGRWRLQ

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATCTTTATTTTTAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCA
GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGTCTTAGCACTGGGGCACTTCTT
GCTTATTTCTTTGGTAGGAAAGGGCTCAGTTTGTCTTGTGGGGTGGTGGCAGGCAGGCCG
GCTTACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG
GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT
TTCTCTAACCTGGCATACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTCTTAGGATCAA
AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCCCTGGCCAGCTTCATTGT
ACATGTGGTGTTCTCTTGTCTGTTCTCTGTAATGTGGTATGCCATGGGGTCTTGCACAAGCCT
TTCCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCTACTTAATATGTAGTC
ATCCTGCAGATTTCAATTCCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
CTTGTTTAATGCTCTCATAAGACCACTTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA
TCTTTATGTGCGTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC
TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCCTACATGTGGTGGGTGCT
CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA
GATGGTGTAGGGCCAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA
TGCAGTCTCTGATTCACTAGGCCCAGGTTGGGCATCTCTAACAACTCCACGTGATGCTGA
TGCTGGTCTATGAACTATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC
TCACACCTATGATCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
TCAAGACTAGCCTGGCCACATGGTGAACCCCATCTGTACTAAAAATACACAAATTAGCTG
GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG
AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAAGGGTGAC
AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA

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FIGURE 168

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234

><subunit 1 of 1, 143 aa, 1 stop

><MW: 15624, pI: 9.58, NX(S/T): 0

MHSLQCPGAATRHHLCVCFSFALALGHFLLISLVGKGLSLSCGVGGRQAGRLIRPWVRR
EGKINFYTINGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL

Important features of the protein:**Signal peptide:**

amino acids 1-28

FIGURE 169

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCAC
 AGGAGTTGAACTGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGCTCCTACTCCTACCTAC
 ATTAATACTGTTTTTTGTCTCTTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGT
 CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC
 ACCGTCCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
 ACCAACTGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAAGGTAGCTGAGCCTCTTGTA
 GCTGCGGCTTTCGAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGAT**TG**ACAAGCCCGAAGATTT
 CATAGGCGATGGCTCCCCTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG
 CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCAT
 CTAACCTTTTCATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG
 AACCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT
 TATGTGACAGGACTTGCAATTCCTTGGAACATGAGGGAACGCGGAGGAAAGCAAGTGCCA
 GGGAAAGAACTTGTGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTTATCACAAGGC
 ATCGAGTCTCCTGCATTAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT
 CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCGATCCACGTACCAGTGCTG
 AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG
 CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAAGTGACCATTTCTCCTCCCCCTCTTCCCTC
 TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG
 GCTCAGTGTTGGCCAGGAGGTGAGCAAGGCCGTGAGAGCTGATCAGAAGGGCCTGCTGTGCG
 AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAGGACTGTGTGGCT
 CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCAAGACCAAAGGAGCTAGAGCTTGGT
 TCAAATGATCTCCAAGGGCCCTATACCCAGGAGACTTTGATTGTAATTTGAACCCCAAA
 TCCAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGTGCTGGCCTGTAATG
 CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGGAGTCAAGACCAAGCCTG
 GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT
 GTGTGCCTGTATCCAGCTACTCGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
 GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
 AAAAATAAAAAAAGAATTATGGTTATTTGTAA

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FIGURE 171

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
CCGCCGCCTCCTGCCCAGCGCC**ATG**ACCCAGCCGGTGCCCCGGCTCTCCGTGCCCGCCGCGCT
GGCCCTGGGCTCAGCCGCACTGGGCGCCGCTTCGCCACTGGCCTCTTCTGGGGAGGCGGT
GCCCCCATGGCGAGGCCGCGGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCTGTGG
CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC
CCTGGAGCAGCCGAGGGGATTTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC
TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC
CTGGCCCTGGCCCTGGCGCTGCCCGCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA
GCCCCCGGAGCTGGGACGGCCCTGTGGAGGACGGCCGAGGCGGAGCACAAGATCGACCTCC
GGCTGAAGCCCGCCTTGGAGACCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC
GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCCTACTACGAGCGCTGCCTGCA
GCTGCTGCGACCCGAGGCATCCTCGCCGTCTCAGAGTCTGTGGCGCGGGAAGGTGCTGC
AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG
GACGTCAGGGTCTACATCAGCCTCCTGCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT
CTAGGGCTGGCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC
CCTGAGTTTAAATTCGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

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FIGURE 172

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQVPVRLSVPAALALGSAALGAATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSRS
MREHPALRSLRLLTLEQPQGDMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCEVDAQPELGRPLWRQAEAEHKIDLRRLKPALETLDELLAAGEAGTFDVAVVDA
DKENC SAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRYIS
LLPLGDGLTLAFKI
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

FIGURE 173

CCGCCGCCGCGAGCCGCTACCGCCGCTGCAGCCGCTTCCGCGGCCCTGGGCTCTCGCCGTCA
 GC**ATG**CCACACGCCTTCAAGCCCGGGGACTTGGTGTCGCTAAGATGAAGGGCTACCCCTCAC
 TGGCCTGCCAGGATCGACGACATCGCGGATGGCGCCGTGAAGCCCCACCAACAAGTACCC
 CATCTTTTTCTTTGGCACACACGAAACAGCCTTCCTGGGACCCAAAGGACCTGTTCCCTACG
 ACAATGTAAGACAAAGTACGGGAAGCCCAACAAGAGGAAAGGCTTCAATGAAGGGCTGTGG
 GAGATCCGAACAACCCCCACGCCAGCTACAGCGCCCTCCGCCAGTGAGCTCCTCCGACAG
 CGAGGCCCCGAGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGGACGATGAGGACCGGG
 GGGTCATGGCCGTACAGCGGTAAACGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCA
 GACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCCCTGGCCTAAAGATGTC
 GGTCTCGAAACGAGCCCCGAAAGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG
 AAGAGGAGAACTCGGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACAGGACTTCACACT
 GAGAAGAAAGCAGCGGTCCGGCGCCACGGAGGGGCCCTCTGGGGGACGGAAAAAAAGAA
 GGCGCCGTGAGCCTCCGACTCCGACTCCAAGGCCGATTCCGGACGGGGCCAAAGCCTGAGCCGG
 TGGCCATGGCGCGGTGGCGCTCCTCCTCCTCTTCTCCTCCTCCTCCGACTCCGATGTG
 TCTGTGAAGAAGCCTCCGAGGGGCGAGGAAGCCAGCGGAGAAGCCTCTCCCGAAGCCGCGAGG
 GCGGAAACCGAAGCCTGAACGGCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGACGAGG
 TGGACCGCATCAGTGAGTGGAAGCGGCGGACGAGGCGGGAGGCGCGAGCTGGAGGCCCCG
 CGGCGGCGAGAGCAGGAGGAGGAGCTGCGGCGCCTGCGGGAGCAGGAGAAGGAGGAGAAGGA
 CGGGAGGCCCGAGCGGGCCGACCGGGGAGGCTGAGCGGGGACGCGCGGACAGCGCGGG
 ACGAGCTCAGGGAGGACGATGAGCCCGTCAAGAAGCGGGACGCAAGGGCCGGGGCCGGGT
 CCCCCTCTCCTGACTCCGAGCCGAGGCCGAGCTGGAGAGAGAGCCAAAGAAATCAGC
 GAAGAAGCCGAGTCTCTAAGCACAGAGCCCGCCAGGAAACCTGGCCAGAAGGAGAAGAGAG
 TGCGGCCCCGAGGAGAAGCAACAGCCAAGCCCGTGAAGGTGGAGCGGACCCCGAAGCGGTCC
 GAGGCTTCTCGATGGACAGGAAGGTAGAGAAGAAGAAAGACCCCTCCGTGGAGGAGAAGCT
 GCAGAAGCTGCACAGTGAGATCAAGTTTGCCCTAAAGGTGCACAGCCCGGACGTGAAGAGGT
 GCCTGAATGCCCTAGAGGAGCTGGGAACCTGCAGGTGACCTCTCAGATCCTCCGACAAGAAC
 ACAGACGTGGTGGCCACCTTGAAGAAGATTGCGCGTTACAAAGCGAACAAGGACGTAATGGA
 GAAGGCAGCAGAAGTCTATACCCGGCTCAAGTCGCGGGTCTCGGCCCAAAGATCGAGGCGG
 TGCAGAAAGTGAACAAGGCTGGGATGGAGAAGGAGAAGGCCGAGGAGAAGCTGGCCGGGGAG
 GAGCTGGCCGGGGAGGAGGCCCCCCAGGAGAAGGCGGAGGACAAGCCAGCACCGATCTCTC
 AGCCCCAGTGAATGGGAGGCCACATCACAAGGGGGAGAGCGCAGAGGACAAGGAGCAGC
 AGGAGGCTCGGGACTCGGAGGAGGGGCCAAGGTGTGGCTCCTGAAGACCTGCACGACAGC
 GTACGGGAGGGTCCCGACTGGACAGGCCTGGGAGCGACCGGACGAGCGCAGAGGGCAGC
 GGGGACTCGGAGGCCCTGGACGAGGAGCT**AGA**CGCCGCGGACAGGAGCCAGCCCGCCG
 CCGAGCTCAGGCTGCCCTCTCCTTCCCGGCTCGCAGGAGCAGAGCAGAGAAGTGTGGG
 GAACGCTGTGCTGTTGTATTTGTTCCCTTGGGTTTTTTTTCTGCCTAATTTCTGTGATT
 TCCAACCAACATGAATGACTATAAACGGTTTTTTAATGA

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FIGURE 174

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD
KCKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDERD
VMAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE
EENSESSSESEKTSDDQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSDSDSVKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV
DRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPAELEREAKKS AKKPQSSSTEPARKPGQKEKRV
RPEEKQQA KPVKVERTKRKSEGFSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNAL EELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV
QKVNKAGMEKEKAEEKLAG EELAGEEAPQEKAEDKPSTDL SAPVNGEATSQKGESAEDEKHE
EGRDSEEGPRCGSSEDLHDSVREGPDLDRPGSDRQERERARGDSEALDEES
```

Signal peptide:

amino acids 1-13

FIGURE 175

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAATTA
 ACACCATTTGAAAGAGAACATTTGTTTTCATCATGAATGCTAATAAGATGAAAGACTTAAAGCCAGAAGCCAAGA
 TTTTTCACCTTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTCTTCAGTCACTGGCACTTTGAAGCA
 AATATTTCCAAGACTCAAGCTAACCTTACAAGAGCTTGCTGCTTTCAAATAGCTGTATTTCCCTTTTTGGGTTTCATC
 AGAAGGACTGGATTTTCAAATCTTCTCTTAGATGAGGAAGAGGCAGGCTGCTTTGGGAGCCAAAGACCACAT
 CTTTCTACTAGCTGTGTTGACTTAAACAAAAATTTAAGAAGATTTATTGGCCTGCTGCAAGGAAGCCGGGTGGA
 ATTATTAATTTAGCTGGGAAGATGCCAATACAGAATGTGCAAAATTCATCAGAGTACTTCAGCCCTATAACAA
 AACTCACATATATGTGTGGAACTGGAGCATTTTCATCCAATATGTGGGTATATTGATCTTGGAGCTTACAAGGA
 GGTATTTATATTCAAACAGACACACATAATTGGGAGCTTGGCAGACTGAAATGTCCTTTGCATCTCAGCAGCC
 TTTTGCTTCAGTAAATGACAGATGAGTACCTTACTCTGGAACAGCTTCTGATTTTCTTGGCAAAGACTACTGCATT
 CACTCGATCCCTTGGGCCCTACTCATGACCACCACTACATCAGAAGTTCGAACTTCAGAGCACTACTGGCTCAATGG
 AGCAAAATTTATTGGAACCTTTCTCATACCAGACACCTACAATCCAGATGATGATAAATATATTTCTTCTTTG
 TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCTTTCTCGAGTTGGAAGAGTTTGAAGAATGATGT
 AGGAGGACAACGCAGCCTGATAAACAAGTGGACGACTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAAG
 TGATGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTATTTACTCCCCACAAGAGATGAAAGAAATCCTGT
 AGTATATGAGGTCTTTACTACAACCAAGCTCCATCTTCAAAGGCTCTGTGTTTGTGTATAGCATGGCTGACAT
 CAGAGCAAGTTTTTAATGGTCCATATGCTCATAAGGAAGTGCAGACCATCGTTGGGTGCAGTATGATGGGAAT
 TCCTTATCCACGGCCTGGTACATGTCCAAAGCAAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCGAAT
 TGATGTCACTCAGTTTTCATAAAGCGGCACCTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGGAGGACCAACGTT
 CAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTCATTTCAGAGAAGTGGCCAGTAGGA
 TGTAAATGTTTCTTGGACAGACATTTGGAAGTCTCCTCAAAGTTGTACAGTCTTTCAAAGGAAGTGGAAATATGGA
 AGAGGTAGTGTGGAGGAGTTGCAGATATTCAAGCACTCATCAATCACTTTGAACATGGAAATGTCTCTGAAGCA
 GCACAGTTGTACATTGGTTCCGAGAGTGGATTAGTTTTCAGCTTCTCTTGCACAGATGCGACACTTATGGGAAAGC
 TTGCGCAGACTTGTGCTTGCACAGAGCCCTACTGTGCTGGGATGGAAATGCATGCTCTCGATATGCTCCCTAC
 TTCTAAAAGGAGAGCTAGAGCCAGAGATGAAAAATATGGCGACCCAATCACCCAGTCTGTGGACATCGCAAGCAG
 CATTAGTCAATGAAGCTGCTGATGAAAGGTGATTTTGGCATTGAATTTAAGTCAACCTTTCTGGAATGTATACC
 TAAATCCCAACAGCACTTATTAATGGTATATCCAGAGGTGAGGATGAGCATCGAGAGGAGTTGAAGCCAGTGA
 TGAAGGAATCATCAAAACGGAATATGGGCTACTGATTCGAAGTTTGCAGAAGAAGGATTTCTGGGATGTATTACTG
 CAAGGCCAGGAGCACACTTTAGTCCACACCATAGTGAAGCTGACTTTGAATGTCTTAGAATGAACAGATAGGA
 AATATCCCAAGGGGCAGAGCATGAGGAGGGGCAGGTCAAGGATCTATTGGCTGAGTCAAGGTTGAGATGACAAAGA
 CTACATCCAAATCCTTAGCAAGCCAAACTTCAGCCTCGACAGTACTGCGAACAGATGTGGCACAGGGAAGACGC
 GAGACAGAGAANAACAGGGGGGCCCAAAGTGAAGACCATGCAGGAATAAGAAGAAGAAAGAAATCGAAGACATCA
 CAGAGACCTGATGAGCTCCTTAGAGCTGTAGCCAGCTAGTTTTCTACTTAATTTAAAGAAAGAAATTTCTTAACCC
 TATAAAAAATGTCCTTCTGTTTGTATATCCCTTATAGTAAATTCATAAATGCTTCCCATGGAGTTTGTCTAAGG
 CAAAGACAATAATCTGAATGAAGACATATGTATGAATATAAGAAAGGCCAAATTCATTTGAACCAATTTT
 CCAAGAACAAATCTTGCAACAGCAAGTATAAGAAATATCCTAAAAATAGGGGGTTTACAGTTTGAATATGTTT
 TTTTGTAGTTTGGAAATTTATTGTCACTGAATAGTTGAGCTAAGCAAGCCGAATTTGATAGTGTATAAGGT
 GCTTTATCCCTCGAATGTCATTAAGCATGGAATTTACCATGCAAGTTGTGCTATGTTCTTTATGAACAGATATAT
 CATTCTTATGAGAACAGCACTACCTTTGTGATGGGAATAAGAGTGCAGACAAATTAAGACAACCTCCATATTC
 AACAGGAATCTTCTCAGTGAAGCCATTCACTCCTGGAGAAATGGTATAGGAATTTGAGAGAGTGTCATTTCTTCTTC
 TGCCACTGGGGTAAATTTAGTGTACTACAACATTGATTTACTGAAGGCACATGATTTTCCCCAGGATTTCT
 ATTGACTAGTCAAGGATTAAGCAGTTTACAGAGAGAAGTTGGTCTTTAGGATATGTGTTTTTATGAGTATATCA
 GCTCTACAGGACAGAACTCTTAATAAATCTTTAATAAGATATGAGGAATAATTTTATAAACAAGAAATAACA
 TAATGATGTATAATGATCTCTGATGGGAAGCATGCAGATGGGATTTGTAAGAGACAGAAGGAAGACGCCAT
 AATTTCTGCTTTTGGGAAACACTCATATCCCATGAAAGGAAGAACATACAAATAAAGTGAGAGTAAATGTAA
 TGGAGCTTTTCTACTAGGTTATAAGTAGCTGCCAATTTGTAATTCATCTGTAAAAAAATCTAGATTTATAACA
 AACTGCTAGCAAAATCTGAGGAACATAAATTTCTCTGAAGATCATAGGAAGATAGACATTTTATTTATAACC
 AATGATATTTCAGTATATTTTCTCTCTTTTAAAAAATATTTATCATACTCTGTATATTTTCTTTTATCTGCT
 CTTTATTTCTCTCTGTATATTGGATTTGTGATTATATTTGATGAATAGGAGAACAATATATACACACAGA
 GAATTAAGAAATGACATTTCTGGGAGTGGGATATATATTTGTTGAATAACAGAACAGGTGTAATTTTAAAC
 AACGGAAAGGGTAAATTAATCTTTTACATCTTCACTCAACCTTTCTCATTTGCTGAGTTAATCTGTGTAAT
 GTAGTATTGTTTTGTAAATTTAACAAATAAAGCCTGCTACATGT

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FIGURE 176

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTyKDLLLSNSCIPFL
GSSEGLDFQTLTLLDEERGRLLLGAKDHI FLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRLGPTHDDHYIRTDISEHYWLNAGAKFIGTFF
IPDTYNPDDDKIYFFFFRESSQEGSTSDKTIILSRVGRVCKNDVGGQRLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPFVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFDDVISFIKRHSVMYKSVYPV
AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVVISKEKWNMEEVLEE
LQIFKHSSIIILNMLSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCCLARDPYCAWDGNA
CSRYAPTSKRARRRQDVKYGDPITQCWDIEDSISHETADEKVIFGIEFNSTFLECIPKSSQQA
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCYCAQEHTFIHTIVKLTLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQLSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKRRNRHHRDLDELPRAVAT
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGCAGAGGT CATCTGGAGCATGCCACC GCGGGGAGCAGA
CAACCTCCCAAGTAAGCTGGGAGCAAGACCTGAAGCTGTTCTTCAGGAGCCTGGTGATATTTTCCCCACCCAC
CTCAGCAGTTTCAGCCAGCAGGAGCTGATCAGGTGTGTCTCTGGAGTGGGAGCAGAAGCGCTGGCTGGCAAGA
GTGGCTCGGAGAAAGAGGTTTCAGCGCTTGACCAGCCGAGCTGCCGTGACTACAAAGTCCAGAAACCTGGGCATC
GGGTGAGGTGGGGGGGACAGGTGTCTATGTGCACCTCTCTTGCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG
AGCCATTGAGGGTGCTATGGAGCTACAGAGGGGAGGGAAAGGTATTTAAAGGTAAAGCTGTGGCACAATAGTTAA
GAGCACAGTTTTTGGAGCTAGACCCACATAGGTTCAAATTTCTCTCTGTGCTTCCTAGTTTCTGTAGCCCCAGGT
AAGGGAGTGACTTAACCTCTCTGGACTTCAATTTCCCTCATCACTAAAGTAGGGCCAAATATAGCACCCACCTCAT
AGGGAAGATTAAATGACATAATGTATGTCTGATGCAACTAGCAAAAGTACCAGTCCCATAGTTCTATGCCCCACAG
TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGGTACTGCAACGACTGGAGCAGAGGGCGCAGAGGCTT
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTCGAGAGAGCATCCGCGGGGACAGGTGAGCC
AGGTGAAGGGGGCTGCCCGCTGCCCTGTCTGCAAGGGGGCTGGCTTAGATGTGAGCGCTGGCTGAAGCCAGCCCA
TGACCCAGGGCCAGGATGAGGTGGAGCAGAGCGGGCGCTCAGTGAGGCTCGGCTGTCCCAGAGGGACCTCTCTC
CAACCGCTGAGGATGCTGAGCTTTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTTTTGAGGAGCCTGCCCC
CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTGGTATTTTCGCTATCAGGCAGGGCGTGAGGATG
AGCTGACAATCACGGAGGGTGAGTGGCTGGAGGTCTATAGAGGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA
ACCAGCAGCGCGAGGTAGGCTTTGTCCTGAGCGATATCTCAACTTCCCGGAGCTTCCCTCCAGAGAGCAGCC
AAGACAGTGACAATCCCTGCGGGGAGAGGCCACAGCATTTCTGGCACAGGCCCTGTACAGCTACACCGGACAGCA
GTGCGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCGCTGCTGCTCGCCCGGGCCAGAGATGGAATAGATACG
GCTTTCTGGAGGGGAGAAATTTGGGGGGCGCTGTGTGGGTCTTCCCTCCCTGCTGGTGGAGAGCTTCTTGGCCCCC
CAGGCGCCCTGAACCTCTTGACCCCTGAACAGATGCTGCCCTGCCCTTCTCTCCAGCTTCTCCCACTGTCAAC
CTACCTCTGTGTGGATGGGCCCCCTGCACCTGTCTGCCCTGGGACAAAGCCCTGGACTTCCCTGGGTTCCTGG
ACATGATGGCAGCTTCACTCAGGCCAGTGCCTGCCACACCTCCCGCCGGCTAAAGCCCGGGATCTTGGCCAC
CAGATCCCTCATCACTGAGGCCAGGAGAGCCTTGACCCCAAGTATGCTGCTGTCCCTATCTCAAGTCTGCAG
CCACACCATCAATGCTCAGAGCAACACAGCCAAAGCTGGAATGCCCTTATTTCCACCTTCCCTCAAGGCT
GGAACTACTGCCCTTCCATTTCTAGAGCTGGAACCCACTCTTTTTCCTATTTGTTATCATCTCTAGACCT
CAGGGCTCACTGGGTTGGCTGGGGAGAGGAACAGGCCCTTGGGAATCAGGACTGGAGCAGGATGCGAAGCAG
CTGTATATGCTCTGAGCGGATTTATTGACAATGAATAAAGGGCAGGAAGGCCAGGCAGGCGCTGGGCTCTTTGT
CTAAGAGGGCAGGGGGCTACGGTGTCTATTGCTTTAGGGGCCACACCGGCGAGGGCTGCTGCCCTGCCAC
GCTCTATCATATGAGCGAGGTTGTGGGAAGGGCGGGCAGGCAGCTGTTGCAAGCAGGGGAGGAGGAGAGAC
TGAGGGGCTGTGACCTCTCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGACTGCTCCCTC
AGCTGGGGGGCAGTGCTGTCCAGTGAGGGGGAGGGCTTTCAGGCCACCCACCCCTGCCCTGCCCTGCGAGT
TCCATCAGCACATTAAGGAGCTTGGAGAAGAGGAAGAATAAACACTTGCTTCTGTCTCAAGCTGTGCCAC
TTTTCCCTGGGGCTCAGAGCACTTCCCTACTCCACCACCAAAACCAAGGGATTATAGCAAAAGCTAAGCTTCA
AGTTTACTCTGGGGTTTCAGGAGGCCAAAGGCTTAATAGTTTAAAGTGAAGTGGGAAGATGAGATTACTTCA
TTTAGGGCTCAGGCAGACTCACCTACATACTCCCTGTCTCCCTGTGGTAGAGACCTGCAGAGAAGGGGAGGGG
TCAACAATGAGAGACAGGAGTAGTCTCTACTGCCCCCAGAGTAGAGACATAGAGCCAGGCCAGGCTGCTC
AGTCCCGCTGTGTTTTCTTACTCTGGTATCAGAAGTGCTGGTTGCTTGGCTGCCATTTGGCTCTTGAAGTG
CGAGCCTGGGCTGGGCGCTCCCTCGGCCCTCAGTGTGGCTCTCGCAAGCTTGGGGTCCCTTCAAGT
CAGAGGGGTAGGCTGCTGTCCCTGAGTCTCCATTCTGTACTGGGGGCTGGCTAGGACTGGGGCTGTGGC
TCTCAGGGGGCAGCCTTCCATGGCAGCATCCTGCTTGGCTGCCCTGCCAGCCCTGACCAACCCCTGCA
GGTCTGTGCCCCACCAAGCCCAAGCTTCTGTCTGTGGGGAGCCATCAGGTTGTCGTGAGTCCATAGCCGT
TCTCAATGTGTCTCACCCGAACCTGGAGGGGAGGGAACACTGGGTTTAGAGACACAATCAGAGGCTGCTT
GCCCTCCCTCTGACCCAGGACATCTGAGTTTGGTGGTACTTCCCTCTGGCTTAAGGTAGGGGAGGCTCTC
AGATTGTGGGACATTGTATGCTGCTGACTCTGCTGGAGCTCCAGCTCAGGAGGAAGAGCCAGGCCACTT
TTGGATCAGGTGCTGATGATGCCCTCCCTACCTCAGCCCCCTTCTCTGGAGCAGCTGCCCCACCTGCGCA
CAGAGAACACAGCTGGTCTCCCTGTCCGGGGGGCGGCTTTTTCTTCTTGGAGCGTCCCTGACGCAAGTGGAG
GCCTCTTGTCTCGGCTGCAATGAGTGAAGGGGCTCAGAGCCAGGTGCACTGTGTGATGATGGGAGGGGGCTC
CGTCTTGCAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGAGGGAGTGAGGGTAACTTTCAATTTCCCT
TCATGTTTTGTTTCTTACGTTTCTTGACAGTGTCTTAAACCCCGGAGGCCCAATTTCCCCAGGCCCAATTT
TTTCTGTGCTTATCTAATAACTCAATATTAAG

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FIGURE 178

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEEFPAPQALATRALPCPAHVVFYQAGREDELTTITEGEWLEVIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSPSSQSDSNPCGAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSSLVEELLGPPGPPPELSDPEQMLPSPSPPS
FSPPAPTSLVDGPPAPVLPGBKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHDPDLT
```

FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGAGGAGAAAGAGACAGAGACAAAGGCACAGCGGAA
 GAGGGCAGAGACAGGGCAGGCACAGAAGCGGCCAGACAGAGTCTACAGAGGGAGAGCCAGAGAGAAGCTGCGACA
 AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAAGCCAGACCCCTGG
 GCACCTCTCCAAAGCCCAAGGACTAAGTTTTCTCCATTTCTTTAACGGCTCTCAGCCCTCTGTAAGAACTTTGCC
 TTGCACCTTGGCAGGAGTCCAAGGCCCCAGGCTACAGAGAGGAGCTTTCAAAGCTAGGGGTGGAGGACTTGGT
 GCCTTAGACGGCCTCAGTCCCTCCAGCTGCAGTACCAGTGCCTATGCCAGACAGGCTCGATCCCGGGAGGGG
 CTTGGAGGGCGCTGGCTGTGGGGAGGCCAACCTGCCTCTGCTCCCATTTGTCCGCTCTCTCTGGCTGGTGTG
 GCTGCTTCTGCTACTGCTGGCCTCTCTCTGCTCAGCCGGCTGGCCAGCCCTCTCCCGGGAGGAGGAGAT
 CGTGTTCACAGAGAAGCTCAAGCGCAGCTCTGCTGCTCGGGCCCTCCGAGGCTGTTGTGCCCTTGCA
 GGCTTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAAGTGCAGGGGCTGACAGTGCAGTA
 CTTGGGCCAGGCGCTGAGACTGCTGGGTGGAGCAGAGCCTGGCAGCTTGGCAGCTCAAGCCATCAAGTAGGATCC
 GGAGTCGGTGGCATCTCTGCACTGGGATGGGGAGCCCTGTTAGGCGTGTACAATATCGGGGGCTGAAGTCCA
 CTTCCAGCCCTGGAGGGAGGCCACCTTAACCTGCTGGGGAGCTGGGGCTCACATCTACGCCGGAAGAGTCC
 TGCCAGCGGTCAAGTCCCATGTGCAACGTCAAGGCTCTCTTGGAGCCCGAGCCCGAGCCCGAAGAGCCAA
 GCGCTTGTCTTCACTGAGTAGATTTGTGGAGACTGGTGGCAGATGACAAGATGGCCGATTTCCACGGTGC
 GGGGCTAAAGCGCTACCTGCTAAGATGATGGCAGCAGCAGCCAGGCGCTTCAAGACCCCAAGCATCCGCAATCC
 TGTCACTTGGTGGTGACTCGGCTGATCTCTGGGTCAGGCAGGAGGGGCCCAAGTGGGGCCAGTGTCTGC
 CCAGACCTTGGCAGCTTCTGTGCTGGCAGCGGGGCTCAACACCCCTGAGGACTCGGGCCCTGACCATTTGA
 CACAGCAATTTCTGTTACCCTGCAGGACTGTGTGGAGTCTCCACTTGGCAGCAGCTGGGTATGGCTGATGTGGG
 CACCGTCTGTGACCCGGCTCGGAGCTGTGCCATTTGGAGGATGATGGGCTCAGTGCAGCTTCACTGCTGCTCA
 TGAACCTGGGTGATGCTTTCAACATGCTCCATGACAACCTCAAGCAGCTGATGATTTGAATGGGCTTTGAGCAC
 CTCTCGCATGCTCATGGCCCTGTGATGGCTCATGTGGATCTGAGGAGCCCTGGTCCGCTGCAATGCGCCCTGT
 CATCACTGACTTCTCGACAATGGATATGGGCATGTCTTTAGACAACCCAGAGGCTCCATTTGCACTGCTCTGT
 GACTTTCCCTGGCAGGACTGATGCTGCTGACCCGAGTGGCAGCTGACCTTCCGGCCCGAGTCAAGCCATTTGCC
 ACAGTCTGGCCGCGCTGTGCTGCCCTCTGCTGCTCTGGCCACTCAATGGCATGCCATGTCCGAGACAACAA
 CTGCGCTGGGCCGATGGCACAACCTTCCGGGCCCGCACAGGCTGCAATGGTGGTCTGCTGCTCCCATGGACA
 GCTCCAGGACTTCAATATTTCCAGAGCTGGTGGCTGGGCTCCTTGGGAGCACTGGGTGACTGCTCTCGGAGCTG
 TGGGGTGGTGTTCAGTTTCTCTCCGAGACTGCAAGGAGCTGTCCCGGGAATGGTGGCAAGTACTGTGAGGG
 CGCCGTATCCCGCTTCCGCTGCCAAGACTGAGGACTGCCAAGTGGCTACGCTTCTCCGCGAGGAGCA
 GTGTGCTGCTCAACACACCGCACCGGACTCTCAAGAGCTTCCAGGGCCCATGAGTGGTCTCTGCTACAC
 AGGCTGGGCCCCAGGAGCACTGCAAACTCACTGCCAGCCCGGAGCTGGGCTACTACTATGTGCTGGAGC
 ACGGCTGGTAGATGGGACCCCTGTCTCCCGGACAGCTCTCGGTCTGTGTCCAGGGCCGATGATCATCTGTGCTG
 CTGTGATCGCATATTGGCTCCAAGAAGAGTTTGACAAGTGCATGGTGTGGCGAGGGAGCGGTTCTGGTTGCA
 CAAGCAGTCAAGCTCTTCAAGAAATTCAGGTACGGATACAACAATGTGGCTCACTATCCCGCGGCGCCACCA
 CATTTCTTGTCCGGCAGCAGGAAACCTGGCCACCGGAGCATCTACTTGGCTGAAGCTGCAGATGGCTCTCTA
 TGCCCTCAATGGTGAATACAGCTGATGCCCTCCCCACAGATGTGGTACTGCTGGGCGACTCAGTCTGCGCTA
 CAGCGGGGCGCTGACGCTCAGAGACACTGCAGGCCATGGCGACTTGGCCAGCTTTGACACTGCAAGTCTCT
 AGTGGCTGGCAACCCCGAGCACACGCTCCGATACAGCTTTCTGCTGCCCGGCCACCCCTTCAAGCGCCAG
 CCGCATCTCCAGGACTGGCTGCACCAAGAGCACAGATTCTGGAGATCTCTCGCGCGGCGCTTCCGCGGGCAG
 GAAATTAACCTCACTATCCCGCTGCCCTTTCTGGGCACCGGGGCTCGGAGCTAGCTGGGAGAAAGAGAGCTT
 GTGTTGCTGCTCATGTAGACTCAGTGGGGAGGGGCTGTGGGCTGAGACTGCCCTCTCTCTGCTCCATCT
 GCGCAGGCTGGCCCTGCCCTGGTTCCTGCCCTGGGAGGCACTGATGGGTTAGTGATGGAAGGGCTGACAGC
 AGCCCTCATATAAAGCTTCCCTTCTGCCCTCGGGTCAAGGAGGAGGGGAGCGAGGAGGCTGGCCCT
 CAGTTGTATTTATTTATTTATTTACTTTTATTTAGCACAGGGAAGGAGCAAGGACTAGGCTCTGGGGA
 CTTGACCCCTGAGCCATACCTCTACCCCTGGGGCTAGGAAATCCAGGCTGGTGTATAGGTATTAAGTGTGTG
 TGTGTATGGTGTGTGTGTGTGTGTGAAATGTGTGTGTGTGTATGTATGAGTACAAGCTGTCTCTCTCTCT
 TTCTCGAATTTATTTTGGGAAAGAAAGTCAAGGTAAGGCTGGGCTTCAAGGACTGAGGAGTATCTTTT
 TTTTTTTCTTTCTTTCTTTCTTTTCTTTTGGAGACAGATCTCGCTCTGCTGCCACGGCTCGAGTGAATG
 GCACAACTCGGCTCACTGACTCTCGCCCTCCGGCTTCAAGTATCTCATGCTCAGCCTCTGAGTAGCTG
 GATTTACAGGCTCTGCGCACACGCCAGCTAATTTTGTGTGTGTGTGGAGACAGACTCTCGCTTGTGTC
 ACCAGGCTGGAATGATTTCACTCACTCAACCTTCCGACCTGGTTCAGCAATCTCTGCTCAGGCTTCC
 CGATGCTGAGATTTATAGCACTACCACACCGCCCGCTAATTTTGTATTTTAGTAGAGACAGGCTTTCAC
 CATGTTGGCCAGGCTGGTCTGCAACTCTGACCTTAGGTGATCCACTCGCTCTCTCCCAAGGTGGTGGAT
 ACAGGCTGAGGCCAGGCTCTGGGCCAGCCCACTAATTTTGTATTTTAGTAGAGACAGGCTTTCACATGT
 TGGCCAGGCTGCTCTGAACTCTGACCTCAGTAACTGACCTGCTCGGCTCTCCAAGTCTGTGGGATACAGG
 TGTGGCCACACCGCCGCTACATATTTTTAAATGAATCTCAATTTATGTAGCTTCTTGGAGTCAGACG

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FIGURE 180

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRLAGRWLWGAQPCLLLPVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV
 FPEKLNSSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP
 GTYLTGTINGDPESVASLHWDGGLLVQLQYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP
 ASGGQPMCNVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHAGLKRILLTVMAA
 AAKAFKHPSIRNPVSLVTVRLVILGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHF
 DTAIFLTRQDLCGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAAHELGHVFNMLHD
 NSKPCISLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
 PVTFFPKDYDADRQCQLTFGPDSSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG
 PAQACMGGRCLHMDQLQDFNI PQAGGWGPWGPWGDSCRTCGGGVQFSSRDCTRPVPRNGGKY
 CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRITDLFSGFPGMDWVPRYTGVAPODQCK
 LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
 SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLAKLPDGSYALNGEYTL
 MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
 PSTPRPTPDQDLHRRALILEILRRRPWAGRK

Important features of the protein:**Signal peptide:**

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
 172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
 582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGG
CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC
AAGAAAATATGTAAATCACTTAAGATTGTGGACTGGTGTGGTATCCTGGCCCTAACTCT
AATTGTCTGTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA
TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAGATTACATGGAAATTGATCCTGTG
ACCAGAAGTAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT
TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA
TTAAAGTGATTCCTGAATTTCTGAACCAGAGAGGAAATAGATGAGAATGAAGAAATTACC
ACAACCTTTCTTTGAACAGTCAGTGATTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
TTTTCTTAAAAATCCAAAATTCTGGAGATTGTGATAACGTGACCATGTATTGGATCAATC
CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT
CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT
AGAGAAGACCCGTACGCCAGACAAGCAAGTGAGGAAGAAGTCCCAATAATGACTATACTG
AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT
CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA
CTGCTACCAAGGAGGACGAGTCATCTGTGTCGTATCATGCCTTGTAAGTGGTGGGTGGCCC
GCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAACTGCTGGCAACATAT
AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT
CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC
AAAAAAAAAAAAAAAAAAAA

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FIGURE 182

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLLIVLFWGSKHFWPEVPPKAY
DMEHTFYSGEKKKIYMEIDPVRTEIFRSGNGTDETLVHDFKNGYTGIFYVGLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWWPAEKPIENRDFLKNKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGEI FDPMLDERGYCCICYCRNRNRYCRRVCEPLLGYYPYCYQGGRVICRVIMPCNWWV
ARMLGRV

Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCGAGGGCCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCCGCACC**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT
 GCTCAGCTTCTTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA
 CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAG
 TGTGTGTGGCACAGCACAGGCATCTACCACTGCCAGATCTACCGATCCCTGCTGGCGCTGCC
 CCAAGACCTCCAGGCTGCCCGGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT
 GCGCCTGCGCCGTCATCGGGATGAAGTGACACGCGCTGCGCCAAGGGCACACCCGCCAAGACC
 ACCTTTGCCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT
 CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT
 GGCACCCCTGCTTTGCCCTGTCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCCGC
 CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACAGCTGCCTACAAAG
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCCTGCTTCTCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC
 AATGGAGGCAGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTGTATCCAAGGAAATA
 ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGAGAA
 AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATAT
 TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT
 TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

FIGURE 185

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG
 CAGGCGGCAGGGCGGGCGGCCAGGAT**CATG**TCCACCACCACATGCCAAGTGGTGGCGTTCCT
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
 GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC
 CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCTCC
 TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAGCC
 AACATGACACTGACCTCCGGGATCATGTTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT
 GTCTGTGTTTGGCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG
 GCATGGGTGGGATGGTGCAGACTGTTTCAGACCAGGTACACATTTGGTGCGGCTCTGTTCTGTG
 GGTGGGTGCGTGGAGGCCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG
 CCTGGCACCCAGAAGAAACCACTACAAGCCGTTTCTTATCATGCTCAGGCCACAGTGTG
 CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAAACCAAAAACAAGAG
 ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTTATCCTTCCAAGCACGACTA
 TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAA
 AACAAGGAGATCCCATCTAGATTTCTTCTTGTCTTTGACTCACAGCTGGAAGTTAGAAAAGC
 CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC
 ACCATAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT
 TTCTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCAC
 ATTTTGATGATTAGACAGACTCCCCCTCTTCCTCCTAGTCAATAAACCCATTGATGATCTA
 TTTCACAGCTTATCCCCAAGAAACTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTT
 CTGCTGTTTGAATTTGTCTCCCCACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA
 GAAGCAATAAGAGAAAGATATTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG
 TGATCTTAAAGTTTACCAAAACCAAGTCATTTTCAGTTTGAGGCAACCAAACTTTCTTACTG
 CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAG
 TCCTCTTTCTGTGCGGGCTCAGAAATTGTCCCTAGATGAATGAGAAAAATTATTTTTTTAAT
 TTAAGTCCTAAATATAGTTAAATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGA
 AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTTGACATTGTCT
 ATATGGTACTTTGTAAGTTCATGCTTAAGTACAAATTCATGAAAAGCTCACACCTGTAATC
 CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGTTCGAGACTAGCCTG
 GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG
 GCATACACCTGTAGTCCAGCATTCGGGGAGGCTGAGGTGGGAGGATCACTTGAGCCAGGG
 AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA
 TCCTGTCTAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAA
 ACTAATTCCTTAA

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FIGURE 186

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAACTGTTCTCTTCTGTGGCACAGAAACCTGCTTCAAAGCAGAAGTAGCAGTTCGG
 GAGTCCAGCTGGCTAAAACTCATCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTG
 GGCTGTTTCTTGGTGGTGTGGAAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG
 AGAGTGTGGCCTTCATTGAAAAACAACATCGTGGTTTTTGAAACTTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGC AAAATCTATGATTCCCTGCTGG
 CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTC
 TTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGTGCACGGGGACAATGAGAA
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC
 TCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT
 GTTGCCCAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGGT
 GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA
 GATACTCGATACGTTCCCATCGCACAAACCAAAAAAGTTATCACCCGAAAGAAGTCACCG
 AGCGCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGC
 CATGCAAATGACAAAAATCTATATTACTTTTCTCAAATGGACCCCAAAGAAACTTTGATTTA
 CTGTTCTTAACTGCCTAATCTTAATTACAGGAACGTGTCATCAGCTATTTATGATTCTATAA
 GCTATTTACAGCAGAATGAGATATTAACCCCAATGCCTTTGATTGTTCTAGAAAGTATAGTAAT
 TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTTATCATTTACTTCAAATGACATTGCT
 AAAGACTGCATTATTTTACTACTGTAATTTCTCCAGACATAGCATTATGTACATAGATGAG
 TGTAACATTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG
 TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAATCATGGATAGGGTTG
 AAGAAGGTTACTATTAATTGTTAAAAACAGCTTAGGGATTAATGTCCCTCCATTTATAATGA
 AGATTAAAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATGAATGGCTTTCTGATATGCTG
 TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTCTCCAGAGGCTTTTTTT
 TTCTGTGTATTAAATTAACATTTTTTAAACGCAGATATTTGTCAAGGGGCTTGCATTCA
 AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG
 GTTTTAGGAAAGTGAAATATTTTTGTTTTGTATTTGAAGAAGATGATGCATTTTGACAA
 GAAATCATATATGTATGGATATTTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC
 AATATAAATAAAAGAGCAGAAAAATATGTCTTGGTTTTTCATTGCTTACCAAAAAACAACA
 ACAAAAAAGTTGTCTTTGAGAACTTCACCTGCCTATGTGGGTACCTGAGTCAAAATTG
 TCATTTTTGTTCTGTGAAAAATAAATTTCTTCTGTACCATTTCGTTTAGTTTACTAAA
 ATCTGTAATACTGTATTTTTCTGTTTATCCAAATTTGATGAACTGACAATCCAATTTGA
 AAGTTTGTGTCGACGCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATA
 TTAATAAATTGTACATTTTCTAATT

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FIGURE 188

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIIVVFENFWEGLWMNCVRQANIRM
QCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TCGCC**AT**GGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGGCTGGGTG
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
CGTGGTGGCCAGGTGGTGTGGGAGGGCCTGTGGATGTCTCGGTGGTGCAGAGCACCGGCC
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
GCCCTCTGTGTATCGCCCTCCTTGTGGCCCTGTTGGGCTTGTGGTCTACCTTGTGGGGC
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCTGGTGTCACTCTGGGA
TTGTCTTTGTATCTCAGGGGTCTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAAGCGGGAGCTGGGGGCCCTCCCT
CTACTTGGGCTGGGCGGCCTCAGGCCCTTTTGTGTGGGTGGGGGGTGTGTGTGCTGCACTT
GCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCCCT
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGCT**CTGAC**CGTGAGGGGAATG
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGCGAGTGCCCAACAGCTTGGGATGGGT
CGTACCTTTTGTCTTCTGCCTCCTGCTATTTTCTTTGACTGAGGATATTAAATTCATTT
GAAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCCCTGG
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC
CAGTCAAGCTATGGAATAATGCGGAGGCTGCTTGTGTGCTGGCTTTGCAACAAGACAGAC
TGTCCTCCCAAGAGTTCCTGCTGTGCTGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG
CCCCCATCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGAAAAACAAATCATCTG
TTAACAAAGGACTGCCACCTCCGGAACCTTCTGACCTCTGTTTCTCCGTCCTGATAAGACG
TCCACCCCCAGGGCCAGGTCCGAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
CTTCTGCCCTGCCCCCCCTCGTCTACCCCTTTTACACTCACATTTTATCAAATAAGCATG
TTTTGTAGTGCA

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FIGURE 190

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736

><subunit 1 of 1, 220 aa, 1 stop

><MW: 23292, pI: 8.43, NX(S/T): 0

MASAGMQILGVVLTLLGWVNLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLALPQDLQAARALCVIALLVLFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKREL GASLYLGWAASGLLLGGGLLCCTCP
SGGSQGPSHYMARYSTSAPAISRGPSEYPTKNYV

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG
AGCATCTTCTACCACTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATTATATCCC
TTGCAAATTGCTGGGCTGGTTCCTGGGTTCTTGGCATGGTGGGGACTCTTGCCACAACCCCT
TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC
TGGGAAGGGCTCTGGATGAAATTGCATCCGACAAGCCAGGGTCCGGTGCATGCAAGTCTTA
TAGCTCCTTGTGGCTCTCCCGCTGCCCTGGAAACAGCCCGGGCCCTCATGTGTGTGGCTG
TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA
GGCTCTAACGAGAGGGCCAAAGCATACCTTCTGGGAACCTCAGGAGTCCCTTTCATCCTGAC
GGGTATCTTCGTTCTGATTCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA
ACCCAGCCATCCACATAGGTGAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA
AGCGCTGCTGCTCTTTCATTGGAGGGGCTGCTTTGTGGATTTTGTGCTGCAACAGAAA
GAAGCAAGGGTACAGATATCCAGTGCCCTGGCTACCGTGTGCCACACAGATAAGCGAAGAA
ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCTTTGGCTCCAAGT
ATGGACTATGGTCAATGTTTTTTATAAAGTCTGCTAGAAACTGTAAGTATGTGAGGCAGGA
GAACTTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGTTGGTAGG
AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAATGCATTGACTATTGTTG
GACCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG
TGTAACAATGATGGACTACTTATTACTTTTGGACCATCATGTATTATCTGATAAGAATCTAA
GTTGAAATTGATATTCTATAACAATAAACATATACCTATTCTA

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FIGURE 192

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop .
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDfYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRRKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV
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Important features of the protein:**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

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FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAGATCACTGGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA
CATACCTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCAC TTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTTAAATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG
AGTTTCTTTCAGTTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTGAGAGTAATCTTG
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
TTTTTTTTTAACACGTCAATAAAAAAATAATCTCCCAGA

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FIGURE 194

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLLCTVVYFCSSEEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNGRVQFLHDGSC**Signal peptide:**

amino acids 1-19

FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC
CGCCGCCATGGCTGCCTCCCCCGCGCGGCTGCTGTCTCTGGCCCTGACCGGGCTGGCGCTGC
TCCTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAAATAAACTCAAGCTGATGCTTCAA
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA
ATTCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGC
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCTACGGCTTTAGGCATGGAGCCAGCG
TCAACTACGATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATT
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGAT
CTTTTCTACCTACTTTGTGTGATCAAAAAGAAGAGTTAAACAACACATGTAAATGCCTTT
TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

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FIGURE 196

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKLKMLQKREAPVPTKTKVAVDENKAKEFL

GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRDRNGHEYIGDYYQRHYD

EDSAIGPRSPYGFRRHGASVNYDDY

Signal peptide:

amino acids 1-30

FIGURE 197

CGGCTCGAGCCCGCCGGAAGTGCCCGAGGGGCCGCGATGGAGCTGGGGGAGCCGGGCGCTC
 GGTAGCGCGGCGGGCAAGGCAGGCGCC**ATG**ACCCTGATTGAAGGGGTGGGTGATGAGGTGAC
 CGTCTTTTCTCGGTGCTTGCCTGCCTTCTGGTGCTGGCCCTTGCTGGGTCTCAACGCACA
 CCGCTGAGGGCGGGACCCACTGCCCCAGCCGTACGGACCCCAACGCCATCCCAGCCCAGC
 GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCAAGCCT
 GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGGTTACAGCAACACCGCCAG
 CCCCAGACTCCCCGAGGAGCCCTCGTGCTACGGCTGAAATTCCTCAATGATTAGAGCAG
 GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG
 GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCTGG
 GCAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC
 CCAAAATCCCCCCTGCCCGCCGGGTCGAGCCCCGGCCCTCCGGGCTGGAATTCGGCAGCCT
 GCTGCTGCCCTGTGCTCCTGTGTTGTGTGCTGCTGGTACTGCCAGATCCAGTACCGGC
 CTTTCTTTCCCTGACCGCACTCTGGGCCTGGCCGGCTTCACCTGTCTCTCAGTCTCCTG
 GCCTTTGCCATGTACCGCCCG**TAG**TGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCTCC
 GGACCTTGCTCCCCGCGCCGCGGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG
 CCTCTTCCGCTGCCCTGGAGCCAGCCCTGCGCCGAGAGGACTCCCGGACTGGCGGAGG
 CCCCGCCCTGCGACCGCCGGGGCTCGGGGCCACCTCCCGGGCTGCTGAACCTCAGCCGCA
 CTGGGAGTGGGCTCCTCGGGTTCGGGCATCTGCTGTGCTGCCTCGGCCCGGGCAGAGCCG
 GGCGCCCCCGGGGCCCGTCTTAGTGTTCTGCCGGAGGACCCAGCCGCTCCAATCCCTGAC
 AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTGCGTGGGAGGCTGGTGAAGGGGAGCGGGAG
 GGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTAAAAA
 AAAAAA

FIGURE 199

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
ATTCCCAGGCTCTCAGAGAAGATCAGCAGAAAAGTCTGCAAGACCCTAAGAACCATCAGCCC
TCAGCTGCACCTCCTCCCCTCCAAGG**ATG**ACAAAGGCGCTACTCATCTATTTGGTCAGCAGC
TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT
GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGG
AAAGCAAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTC
TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCA
CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAGGCATCCACTGCGCAAAAAGGA
TTGTGTCCGGAGCACGGGGGATGAACAACCTGGGTAGAATGGAGGTTGCACTGTTCAGGCCGG
CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGA**TGA**AACAGGGTGCGGGTGCACCGTGG
AGTCATTCCAAGACTCCTGTCTCACTCAGGGATTCTTCATTTCTTCTTCTACTGCCTCCA
CTTCATGTTATTTTCTTCCCTTCCCATTACAACTAAAACAGCCAGAGCCCCAGGAATAAA
TGGTTTTCTTGGCTTCTCTTACTCCATCTGGACCCAGTCCCTGGTTCCTGTCTGTAT
TTGTAAACTGAGGACCACAATAAAGAAATCTTTATATTTATCG

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FIGURE 200

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop .

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI

NENADGSFDYGLFQINSHYWCNDYKSYSENLCNVDCQDLLNPNLLAGIHCARRIVSGARGMN

NWVEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTGACGCCCTGCTTGACTGAGAACCCA
 CCAGCTCATCCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACACCTGAG
 CAGAATGGAATCATTATTTTTTTTCCCAAGGAGAAACCGGGTAAAGGGAGGGAAGCAATTC
 AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAGAAATCCACTCAGAGAGGAC
 TTGGGGTGAACCTTGGGTCCTGTGGTTCCTGATTGTAAGTGGAAGCAGGTCTTGCACACGC
 TGTTGGCAAAATGTAGGACCAGTTAAGTGACTGGCAGAAAAAATTCAGGTGGAACAAGCA
 ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC
 CTGTTGCATTTGGCAAGTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATG
 CAGACTCCAGTTCTCCTGCTGCTCCTGATGCTGGGATGCGTCCGTGATGATGGTGGCGATGT
 TGCACCCCTCCCCACCACACCCCTGCACCAGACTGTACAGCCCCAAGCCAGCAAGCACAGCCCT
 GAAGCCAGGTACCGCTGGACTTTGGGGAATCCAGGATTGGGTACTGGAAGCTGAGGATGA
 GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTCACTGCGGGAGGATCAGC
 TGCTGGTGGCCGTGGCCCTTACCCAGGCCAGAAGGAACAGAGCCAGGGCAGGAGAGGTGGG
 AGCTACCGCCTCATCAAGCAGCCAAGGAGGAGGATAAGGAAGCCCCAAAGAGGGGATGGGG
 GGCTGATGAGGACGGGAGGTGCTGAAGAAGAGGAGTTACCCCGTTGACCGTTGGACCCAC
 GTGGCTCCAGGAGGCCTCAGTGCCCGCATCCCCCTCCAGAGGCTGTGCCGAGGTGCGG
 CACCACCTGTGTCTGCAGCAGCACCCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG
 TTTCCATGATGAGGCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC
 CCAGGGCCTTCTGAAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTCAAG
 TCTGCTCTCAGCAATATGTGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG
 GCTGGGTGCATCAGGGCCGGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT
 TCAATGGATGCCACTGCGAGTGCCACCAGGCTGGCTGGAGCCCTCCTCAGCAGAATAGCT
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA
 TTACCCCTCAAAGGACCTGCACGCTGGGGTGTGGACTGGAAGCTGGATTTCCTCAGGAAAC
 CTTTGCCAGAGCATGTAGGAAAGGCCCTCCAGTCCCCCATAAAGCCCCATCAGGAGCCCTGTG
 GTGCCCGGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAACACTGGAGCGTATGACTC
 TCTTATGTGCTGCGAGGTGGTGAACACCTCGAAGTGTCTTTCAAGGCCTGGCTCTGTGGTG
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAAATCAGGATTCCTCAT
 TCCCCCTCGACCAGGAGGCCACCCTGAGGAACAGGGTTTCGATTGCTGAGACCTGGCTGGG
 GTCAATCAAAGAAACCTTCTACAAGCATAGCCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGA
 AGCCAGACTGCTGCAAGCCTTGCAGCTGCAAAGGAGACTGGGTGTGCGGACATTCCACTGG
 TTTCTGGCTAATGTCTACCCCTGAGCTGACCCATCTGAACCCAGGCCAGTTCTCTGGAAA
 GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAGGGGACATCCTGGGCT
 GTCCCATGGTGTGGCTCCTTGCAAGTGACAGCCGCGCAGCAACAGTACCTGCAAGCACACAGC
 AGGAAGGAGATTCACTTTGGCAGCCCAAGCACCTGTGCTTTGCTGTGACGCAGGAGCAGGT
 GATTCTTCAGAATCTGCAGGAGGAAGGCCTGGCCATCCACCAGCAGCACTGGGACTTCCAGG
 AGAATGGGATGATTGTCCACATCTTCTGGGAAATGCATGGAAGCTGTGGTGCAAGAAAC
 AATAAAGATTTGTACCTGCGTCCGTGTGATGGAAGAACCCGCCAGCAGTGGCGATTGTGACCA
 GATAAATGCTGTGGATGAACGATGAATGTCAATGTGAGAAGGAAAGAGAATTTTGGCCATC
 AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTTCATGAAGCTGATCCTTTTGTGT
 GTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAAGAATAGGAAGTTTCTCCTTT
 TCACACCTTATTTTCATGACTGTGGCTGCTTA

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FIGURE 202

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
><subunit 1 of 1, 639 aa, 1 stop
><MW: 73063, pI: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTVAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEESPLEGLPPFISLREDQLLVAVALPQARRNQSQGRGGSYRLIKQPR
RQDKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDLVLFMDAHCECHPGWLEPLLSRIAGDRSRVSP
VIDVIDWKTQYYPSKDLQRGVLDWKLDHWEFLPEHVRKALQSPISPIRSFVVPGEVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIYQNQDSHSPLDQEATL
RNRVRIAETWLGSKFKETFYKHSPEAFSLSKAEKPDCEMERLQLQRRRLGCRTFHWFLANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQYYLQHTSRKEIHFGSP
QHLCFAVRQEQVILQNCTEEGLAIHQHWFQENGMIVHILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER
```

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGACATGGA
 GTCCAGGATGTGGCCTGCGCTGCTGCTGCCACCTCCTCCTCTCTGGCCACTGCTGTTTGC
 TGCCCTCCACCGCTGCTCAGGCTTTCATCCTCCCTCGAACCCTCCAGCCCGAGCC
 CGCCCCCGTGTGCCAGGGGAGGCCCCCTCGGCCCCACGTCATGTGTGCGTGTGGGAGCGAGC
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTGCGGCAAGTCTGCTGCGCACTG
 CACCCCCAGCCACCCATCAGGCTTTGAGGAGGGGCGCCCTCATCCCAATACCCCTGGGCT
 ATCGTGTGGGGTCCACCGTGTCTCGAGAGGATGGAGGGGACCCCACTCTGCCAATCCCGG
 ATTTCTGGACTATGGTTTTGACGCCCCATGGGCTCGCAACCCACACCCCACTCAGACT
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGAGAGGGCACTGCCACCCCTGGGGCACTTC
 CTGTTGCGGGGCGGTGGGGAAGGTGTGGACCCCCAGCTCTATGTGACAATTACCATCTCCAT
 CATCATTTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC
 GACGCAGACCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGGCCAGCAGCCACTGACA
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCTTCGGGGACTCACCTACCCCCACCC
 TGACCATGAGGAGCCCCGAGGGGACCCCGGCTGGGATGCCACCCCAAGGGGGCTCCAG
 CCTTCCAGTTGAACCGGTGAGGGCAGGGGCAATGGGATGGGAGGGCAAGAGGGGAAGGCAAC
 TTAGCTTTCAGAGCTGGGGTGGGGTGGCCCTCTGGATGGGTATGAGGAGGCAGGCGTGGC
 CTCCACAGCCCCCTGGCCCTCCCAAGGGGCTGGACCAGCTCCTCTCTGGGAGGCACCCCTTC
 CTTCTCCAGTCTCTCAGGATCTGTGTCCTATTCTCTGCTGCCATAACTCCAACTCTGGCC
 TCTTTGGTTTTTTCTCATGCCACCTTGTCTAAGACAACCTGCCCCCTTAACTTGATTCCC
 CCTCTTTGTCTGAACCTCCCCCTTCTATTCTGGCCTACCCCTTGGTTCTGACTGTGCCCTT
 TCCCCTTCTCTCAGGATTCCTCTGGTGAATCTGTGATGCCCCCAATGTGGGTGCAAGC
 AAGCAGGAGGCCAAGGGGCGGCACAGCCCCATCCCACTGAGGGTGGGGCAGCTGTGGGGA
 GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCTTGCACACCACCCGGAACACTCCCCAGCC
 CCAGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCTCACATATCTGTGACTTCG
 GGTCCCTGTCCCCACCCCTGTGCACTCACATGAAAGCCTTGCACACTCACCTCCACCTTAC
 AGGCATTTCGACACGCTCCTGCACCTCTCCCGTCCATACCGTCCGCTCAGCTGACTCT
 CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCCACATTCTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTTCTGCACTTTACCTCTCATGTGCGTTTCCCAGGCTGATGTTGTGGTGG
 TGTGCGGCGTGCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGAGCCCGCTGC
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGCTCCTTGGGCCCCATCGGTGATGG
 TCTGTCCTTCCATCCACACCAATTGTTTCTCTGTCTCCCCCTCACTCCAAGATGCCGCA
 TCACCCCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCCAGCCCA
 CTGTGTAATAATCTGTTTTCTGACAGATGGGTTTGGGGAGTGCCTGCTGCACTACATGAGAA
 AGGGACTCCCATTTGCCCTTCCCTTTCTCCTACAGTCCCTTTTGTGCTGTCTGCTGCTGCTG
 TCTGTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCCTTCCCTTCCAGCCT
 CCTTTGGGCTCCCTAACTCCACCTAGGCTGCCAGGACCGGAGTCACTGTTTCAAGGCC
 ATCGGAGCTCTGCTCCAAAGTCACTACCTTCCCTTCCCGGACTCCCTGCTGCTCCCTTCTT
 CCTCCCTCCTTCTTCACTCTCCTTCTTCTTCTGCTTCCCTGCCCCCTTCCCTCCTCAGGTT
 CTTCCCTCCTTCTCACTGGTTTTTCCACCTTCTCCTTCTTCCCTGCTGCTCCTAGGCT
 GTGATATATATTTTTGTATTATCTCTTCTTCTTCTGTGGTGATCATCTGAATTACTGTG
 GGATGTAAGTTTCAAAATTTTCAATAAAGCCTTTGCAAGATAA

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FIGURE 204

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGFAASFQRLRGLLLLLLLQLPAPSSASEIPKGGKQKAQLRQREVVDLYNGMCLQGPGAV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTFPNYQCSSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

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FIGURE 205

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGATGG
 CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCCCTGCGGTG
 CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
 GTCGGGAGAAGCCCCCGTGGAGAGCACACGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC
 CAGCCCCCACCCTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC
 GCGGGTCTGCTGGGGCCCGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG
 CGTGCTGCTGGCGCTCGTGGTCTGTCGCGCTGAGAAAGTTTTCTGCCTCCTTGAAGCGAATAAA
 GGGGCCGCGCCCGCGCGCGCGACTCGGCAAAAAAAAAAAAAA

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FIGURE 206

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVVESTSPGREPVDTG
PPAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

GGCCGTTGGTTGGTGC GCGGCTGAAGGTTGTGGCGCAGACAGCGTCGTTGGTTGGCCGCGG
 CGGGCCGGGACGGGC**ATG**GCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA
 CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATTGTGA
 ACTTCAAGTCTGTGGTGGTGGGCGACATCCCCGTGT CAGGGGCGCTGCTCACCGACTGGAGC
 GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA
 CCAAGTGGCGACAGAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC
 CCGGGTATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC
 GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG
 ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGGGGACCTCCCC**TAA**GTAGCCC
 CCAGAGGCGCTGGGAGTGTGGCACCGCCCTCCCTGAAGTTTGCTCCATCTCAGCTGGGG
 GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACAGGCCGAT
 CGACTGT CAGCACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAAGTGCACAG
 ACTCGCACGTGCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCACCCGT
 GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGAGGGGGGCTCCCCGCTTCCAC
 CTGGCTGT CATCGGTTAGGGCGGGGCGTGGGTT CAGGGGCGCACC ACTTCCAAGCCTGTGT
 CCCACAGGTCTCGGCGCAGTGGAAAGT CAGCTGTCCAGGGCCTCCTGAACACATAAATAAC
 TGGCACAAGTAAGTCCCCCTCTCAAACCAACAGGCAGTGTGTGTATGTGAGCACCTCGTG
 GGTGAGTATGTGTGGGGCAGAGGTGGCTCCCTCAGCTCCCACGTCTTAGAGGGGCTCCCGA
 GGAGGTGGAACCTCAACCAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAG
 GTCTCCGACCTCAGCTGGAGGCGGGCATCTTTCCTAAAGGTTCCCATAGGGTCTGGTTCC
 ACCCATCC CAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC
 ATGGAGGGGCTGACTGCCCCACATTGCCCTTTCAGACAGGACGAGCATGAGTTAAGCCGCG
 CCTGACCTGGACTT CAGGGGAGGGGGTTAAAGGGAGAGAGAGGGGGGCTAGGGGGTCTCT
 AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC
 CTCTGCAACCACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG
 CCTGGGACACACAGAGCCACCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA
 AGGGGTGCTCGTAAGCCAACACAGCGTGC CGCGGCCTGCACACCTTCGGACATCCAGGC
 ACGAGGGTGTGCTGATGTGGCCACATAGGACCACAGCTCCCAGCTGGGAGGAGAGGCCT
 GGGGCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
 CCGCAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT
 TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCGAGGGCAAC
 GTGGGGCGGAGACTCAGTGGACAGCCCTGCCTGTCACTCTGGAGCTGGGCTGCTGCTGC
 CTCAGGACCCCTCTCCGACCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG
 GAGGGAATGGGGTGGGCTGTGCGCAGCATCAGCGCTGGGCAGGTCCCGCAGAGCTGCGGGA
 TGTGATTAAAGTCCCTGATGTTTCTC

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FIGURE 208

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK
ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER
HLAPGSWGGQLSREGPSLAPEGSMPSPRGDL P

Signal peptide:

amino acids 1-15

FIGURE 209

AGCAGGAGCAGGAGAGGGGACA**ATGGA**AGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTCTCT
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCCTG
 GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCC
 ACTGAGGTGGCTGTCTATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA
 TAGCATGGTGCAAAAATTTCCAGGCGTGTCATTTGGGATCAGCACTGATTCTGAGGTTCTGA
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACTG
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT
 CAACAGCCTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCG
 TAATTCAGATTTCCTCTCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG
 CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTCAAACATAAAGGAGTCTCAACTGCCAG
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTTCC
 GTAGAGCATGTGCAAAACTTTTGTGATGGATTCCCTAAGTGGAAAATTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAAC**CTGA**CTTCTCTTGGAACTACATATGGCC
 AAGTATCTACTTTTATGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG
 GATCACTAGGCCTGCCAACACACACACACGACGTCACACACGACGACGACGCGTGCACAC
 ACACACGCGCACACACACACACACAGAGCTTCATTTCTGTCTTAAAAATCTCGTTTTCTC
 TTCTTCCTTCTTTTAAATTTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGT
 TTGTATACTGCACATGACTTACACACAACATAGTTCCTGCTCTTTTAAAGGTTACCTAAGGGT
 TGAAACTCTACCTTCTTTCATAAGCACATGTCCGCTCTGACTCAGGATCAAAAACCAAAGG
 ATGGTTTTAAACACCTTTGTGAAATTGTCTTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCATGCTTGGTTAGCATCTCCAACCTCC
 TATGTAATCAACAACCTGCATAATAAATAAAAGGCAATCATGTTATA

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FIGURE 210

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPWLTDPAAEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA
KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDWDTLPTAEVSVQHVQNF
CDGFLSGKLLKENRESEGKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGAGAGTGCCACCCGCGCGGGTG
 GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
 GACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACGATGGCAGCGTCCGCCGGAGCCGGG
 GCGGTGATTGCAGCCCCAGACAGCCGCGCTGGCTGTGGTCGGTGCTGGCGGCGGCGCTTGG
 GCTCTTGACAGCTGGAGTATCAGCCTTGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA
 ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC
 TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTGCTTTTTTCCACTACTC
 CCAAGGGCAAGTGTAACCTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAG
 ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAAATATGCAGTTTATACACAATGGCACC
 TATATCTGTGATGTCAAAAACCCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA
 TGTGCTAGAAAAAGAGAATTTGGCTGTGTTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG
 CTGTGGTCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA
 AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTTGTACCAGTTAAGCAGGC
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC
 AGGGCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC
 AAGTCAGAGTCTGTGGTGATGCGGATATCCGAAAGAATTAAGAGAATACCTAGAACATATC
 CTCAGCAAGAAACAAACCAAACTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT
 AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT
 ACAAGGATATGTATAAATATTTCTATTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGA
 TGAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTCTTTTC
 AGGTCATTACAAATTGGGAGATTTCAGAAACATTCCTTTTACCATCATTTAGAAATGGTTTG
 CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG
 GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGAA
 GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTATTTGTCTGCCGCTTTTAAAA
 AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT
 AAAATATGGGGCAATTGTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCCTTG
 AAATGTGTATATCAATTTCTGGATTCAATAGCAAGATTAGCAAAGGATAAATGCCGAAG
 GTCACTTCATTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAAATCCAAGCTTTGCTT
 GAGAACTTTTGTAACTGGAGAGTAAAAAGTATCGGTTTTTA

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FIGURE 212

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKASINIEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDTGCTSESLSVPKQAPRKSPSDTEGLVKSLPSSGSHQGPVIYAQLDHSG
GHHSKINKSESVVYADIRKN

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

FIGURE 213

GCCGGCTGTGCAGAGACGCC**ATGT**ACCGGCTCCTGTCAGCAGTGACTGCCCGGGCTGCCGCC
 CCCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGTCCATCAGCGCGCCGGGCTGCCGCC
 TCTCGGCCACGGCTGGGTGCGGGGCCCTCGGGCTGGGGCTGGGGCTCGGGGTGAAGC
 TGGCAGGTGGGCTGAGGGGCGCGGCCCGGCGCAGTCCCCCGGGCCCCGACCTGAGGCG
 TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGAGACCCCGGC
 GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCGCGACCTGCTGCACAGGA
 TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAGAAGTC
 TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG
 CAGGGAAACTGGATCTTGATATTCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCATTAAAGTGAATTCG
 TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAGCCTTGAAGATGA
 TGAAGAGAATGTTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGATGATTTT
 ACTAAATTTAAAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAA
 AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTGAAAATTCATTGAAT
 CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA
 ACTTTTGGCTATACCCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTGGA
 CTATATGCAGAAAATATTCCATGACTTGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
 CAGTGATTTACAATAGAGCAAGG**TAA**ATGAATACCTTCTGCTGTGCTAGCTATATCGCATC
 TTAACACTATTTTATTAATTAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC
 CACATTTTGGGAGCTTTTCTACATGCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAAAACA
 TGTTTATAAAGTAAAAAA

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FIGURE 214

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLGALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQESLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLMLTTVQEENEPVIYNRRAR
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG
 AGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGCAGCGGCTGCCGGCCGGGACT
 GGTGCGGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT
 GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT
 GGAACCAGCAGGATGGTACCTTGTCCTGTACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC
 CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG
 TGGAGTCGCACCTGTGCGGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC
 GTGTGCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAAGGCCAAGAACCCCCAGGAGCAGAAG
 TCCTTCTTCGCCAAATACTGGATGTACATCATTCCCGTCGTCTGTTCTCATGATGTCAGG
 AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC
 TTTGCTGTGTGCCACCCTCCCTGTAAAGTCTATTTAAAAACATCGACGATACATTGAAATGTG
 TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG
 TCCTGATGTACAAGCTTGATTGAAATTCAGTGCTCACTTGATACGTTATTCAGAAACCCAAG
 GAATGGCTGTCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT
 TAACTGTGTCGCCAGATCGACACGCAAAAAAAAAA

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FIGURE 216

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
 DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIPIRRPGALDGLEA
 GGYVSSFVPACSLVESHLSQTLTHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
 LQPPTTAPGPETAFAFIERLEMEQAQKAKNPQEKSFFAKYWYIIPVVLFLMMSGAPDTGGQ
 GGGGGGGGGGSGLCVPPSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCCT
 GGAGCCGGACGTGTCCGGGGCGTCCCCGCAGACCGGGGCAGCAGGTCTCGGGGGGCCACC
ATGCTGGTGACTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGAAC
 GTCAAGATGCCGGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTTCGGTTTC
 AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
 CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG
 TGGCCTTGCCCTCTACAGTCCTCTTTGGCCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTG
 GCAAGAATTCTTGTGCTCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACTCTCT
 CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT
 GGATCCAGCTACCTTTGTCTGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCTGTAGCGCCCTTTGTGGCTGC
 CATCCCTCTCCTGGCTCTGGCAGGGGCCTTGGCCCTTCGAAACTGGGGGGAGAATATGACC
 GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGTGCGGACCGCCG
 GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGTCTCTCATCTTTGTCTTCCT
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGGCATTATCTTCTCCAGCTTCATGG
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG
 CCCATGCACCTGCTGTCCCTTGCTGTGCTCATCGTCGTCTTCTCTCTTCATGTTGACTTT
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTTCATAGCCTTTCTACTTATTGAGT
 TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA
 GAGCAGGCTGGTGTACTCAACTGGTTCGGGTACCTCTGCACTCACTGGCTTGCCCTAGGGCT
 CCTTGCTCCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTGACATTGTCTCTG
 CTGTCATGGTGTGAGCTCTGCTGGCAGTGGTGGGACTCTTACCGTGGTAAGGCATGATGCT
 GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCTGAGCTGTAAACCCCACTCCAG
 GACAAGATAGCTGGGACAGACTCTTGAATTCAGCTATCCGGGATTGTACAGATCTCTCTGT
 GACTGACTTTGTGACTGTCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA
 TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAAGTTCCCTCTGTGTTACTCCATTAGAAA
 ATAAACACTTTTAAATGATCAAAAAAAAAA

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FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDIFYQVYFLALAADWLQAPY
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR
VLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGII FSSFMAASLLGSSLYRIATSKRYHLQ
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPMSFLLRRKVIPET
EQAGVLNWFVRVPLHSLACLGLLVLHDSRKTGTRNMF SICSVMVMALLAVVGLFTVVRHDA
ELRVPSPTTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
314-330, 343-359, 379-394, 410-430

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FIGURE 219

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCGGGCGGGCCCGGCCCTGGAG**ATG**
 GTCCCCGGCGCCGCGGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCCTCGCGGCCCA
 CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACA
 TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
 CACCTTGTCCTCCGCTGAACCTCCAGAGGCCTGCGGGGAACTCAGCAACGGTTTCTTCATCCA
 GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCC
 AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGG
 CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT
 CCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
 TGGT**TAGA**AAGAGTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
 AGGAATTTTGTACTTTGGAATTTGGAGATAGCATCTGGGGACAAGTGAGCCAGGTAGAGGA
 AAAGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG
 GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA
 GAACCCGAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT
 CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG
 AGTGGTTTAAAGAGCTGGTGGTTTGGGGACTCAATAAACCCCTCACTGACTTTTTAGCAATAAA
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 220

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRINDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

Signal peptide:

amino acids 1-20

[illegible]

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FIGURE 222

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCgiYKDNnkSSIHCMDLSQRYCLMAVFNVIYLENEDSE

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTTCTTCTGGATGGGGGCCAGGGGGCCAGGAGAGTATAAAGGCGATGTGGAG
GGTGCCCGGCACAACCAGACGCCAGTCACAGGCGAGAGCCCTGGGATGCACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTTAGCACCCTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTTCTCCTGGTAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTTGTCGCCTTCCAAGCTTTCTCCGGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC
AGCAAACCTACCCGTGGGTCGC~~TAG~~GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCAGAAA

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FIGURE 224

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVK
LGDSWDVKLGALGGNTQEVTLQPGEYITKVVFVAFQAFLRGMVMTSKDRIFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYANSPPVGR
```

Signal peptide:

amino acids 1-22

FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCCTTCTGGGCTCCAACGCAGCTCTGTGGCT
 GAACCTGGGTGCTCATCACGGGAACTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
 CCCCAAATTGGCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTT
 TTTTTTTTAAACCGCCCCCTCCCCACCCCCCAAAAACTGTAAAGATGCAAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT
 TATTTGTTCTTGGAGTGTTCTGCGTGGCTGGCAGGAATAATGTTCCAAAATCGGTCCATCT
 CCAAGGGGTCCAATTTTTCTTCTGGGTGTGACGAGCCCTGACTCACTACAGTGCAGCTG
 ACAGGGGCTGTCTGCAACTGGCCCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAA
 CAATACAAAGGATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCCTGCTTACTGACAATGCTTCTTCTGCGGAAACGAGGATGCCCTAAGGGCTG
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGTATAACAGCCTTCAAAAACCTAAGTATAAT
 CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT
 TGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA
 TCTCCTATTTTCTTAAACAATACCTTCAGACCTGTGACAAATTTACGGAACCTTGGATCTGTCC
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTT
 ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC
 TGGAACCTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC
 ATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTCCAAGCTCAACCTGGCCCT
 TTTTCCAAGGTTGGTCAAGCCTTCAAGACCTTTACTTGCAGTGGAAATAAAATCAGTGTCTAG
 GACAGACCATCTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATC
 GAAGCTTTCAGTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGA
 TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGATATCCCTCAATGACA
 TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTCTCCCTTGTAACCTGGCTG
 AAAAGTTTTAAAGGTCTAAGGGAGAATACAATATCTGTGCCAGTCCCAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCACTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGT
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCCAGGCCGAGCAT
 GAGAGCAAAACCCCTTTGCCCCGACGGTGGGAGCCACAGAGCCCCGGCCAGAGACCGATG
 TGACGCCGAGCACATCTCTTTCCATAAAATCATCGCGGGCAGCGTGGCGGTTTTCTGTGCCG
 TGCTCGTATCCTGCTGGTTATCTACGTGTCTGGAAGCGGTACCTGCGAGCATGAAGCAG
 CTGCGACGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAACAGCTCCCTAAAGCAAT
 GACTCCCAGCACCCAGGAATTTTATGTAGATTATAAACCCACCAACAGCCGAGCCAGGAGA
 TGCTGCTGAATGGGACGGGACCTTGCACCTATAACAAATCGGGCTCGCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAAGAGCTCTTAAAGCTGGGAATAAGTGGTGCTTTATTGAACTC
 TGGTGACTATCAAGGGAACCGCATGCCCCCCCTCCCTTCCCTCTCCCTCTCACTTTGGTGG
 CAAGATCTTCCTTGTCCGTTTTAGTGCATTATAATACCTGGTCATTTTCCTCTCATACATA
 ATCAACCCATTGAAATTTAAATACCACAACTCAATGTGAAGCTTGAACCTCGGTTTAATATAA
 TACCTATTGTATAAGACCTTTACTGATTCCATTAATGTGCGATTTGTTTTAAGATAAAACT
 TCTTTCATAGGTAAAAA

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FIGURE 226

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTLLTMLSSAERGC PKGCRCEGKMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRI FQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKEHLHLEHNQFSKLNLA LFPRLVSLQONLYQWNKISVIGQTM
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLD SNKLTFFIGQEILDSWISLNDISLA
GNIWEC SRNICSLVNWLKSFKGLRENTI ICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKFPPLPPTVGATEPGPETDADA EHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKRQSLKQMPSTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCTATCCTAAGTTGACTGTCCTT
TAAAT**ATG**TCAAGATCCAGACTTTTCAGTGTCACCTCAGCGATCTCAACGATAGGGATCTTG
TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT
AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCCTCTGCTGCTGGTTTTTGG
TGGCAGCTCTTCTCTGTGGAGCTGTGGTCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA
ATTGATTCTCACAGGCGCACCATGGCAGTTTTTGCTGTTGGAGACTTGGACTCTATTTATGG
GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTCAAACCTCAAACCCCTGACCTAT
ATCCTGTTCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
AAAACAACCT**GA**TTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA
AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATA
GTCTGAGGAAGGACAATTTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATG
TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC
AACCAAATTAATGCTTCTCCACTAGTATCCAACAGGCAACAATTAGGTGCTGGAAGTAGTT
TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC
CTAGCATGGGGTCCATAAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT
GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
CAGCAAAAACAAGAGGTTTTATGCCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC
CTTTTACAGTAATGAATGTGGCTCCATAGTCCATAGTGTCTCTGAGGCTCAGGGCTTG
GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC
AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA
CAAAAACATCCATACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT
AAACATCAATAGATATCTAAAAA

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FIGURE 228

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSIAISTIGILCLPLFQLVLSDFCEEDEMCVNYNDQHPNGWYIWILLLLVLVA

ALLCGAVVLCLQCWLRRPRIDSHRRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP

VPAPCFGPLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGCGGAGTAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGACAGCTGACGCCCGCTTATTA
 GCTCTCGCTGCGTCGCCCGGCTCAGAAGCTCCGTGGCGCGGCGACCCGTGACGAGAAGCCCC
 ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCCCTTTTAAACT
 CCCTCTTCAAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACACCTTGCTGAAG
 ATGAAGAATATACAATATTGAGGATATTTTTCTTTTTTTTTTCAAGTCTTGATTGTGGC
 TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTGTTCTTCAGAAATGTTTTTTA
 CAATCTCAAGAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGTATTTGGACTCATT
 TGGGGATTGATGTTTACTGCACATATCTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
 ACGTGAGCAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAAATAAGA
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATT
 GCTGTCCTTCTGGATGACATTTTGCAACGATTGTTGAAGCTGGAGAACAAGTTGACTATAT
 TGTGTGAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA
 CCACAAATAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTGC
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAAATTGCTGGCTTAGGAC
 AGAGCAATACTTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTGATGGAAC
 TCTAATTCTGTACATAAAAATTTTAAAGTTATTTGTTTGGCTTTCAGGCAAGTCTGTTCAATG
 CTGTACTATGTCCTTAAAGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGT
 TTTGTATAAATCTTTTGTGTTTGGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTCT
 ATTTCTATAACACATTTTATTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTTAA
 TCATTCTGTCATTTGTTCTCAATAGATGTAACGTGTAGACTACGGCTATTTGAAAAATGTG
 CTTATTGTACTATATTTTGTATTTCGAATTATGAGCAGAGAAAGGAATATAATGTGAAAA
 TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTTGCACATATCCTTCAGAATAACTGA
 AGGTAATTATTGTATATTTTTAAAAATTACACTTATAAGAGTATACTTGAATGGGTAG
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTTAAATAGTT
 GTAACTCTAATCTTATACTTATTGGAAGAATAAAAGATATTTTATGATGAGAGTAACAATA
 AAGTATTCATGATTTTTTACATACATGAATGTTTCATTTAAAAGTTTAACTCTTGAGTGTCT
 ATGCTATCAGGAAAGCACATTTATTTCCATATTTGGGTTAATTTTGCTTTTATTATATTGGTC
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTGAGGACTTAGCCAGGTGTATATAATAAA
 GGTACTTTTGTGCTGCATTAAATTGCTTGGAAAGTGTAAACATTATATTATATAAGAGTATC
 CTTTATGAAATTTGAAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC
 TTAATAATAAGAACATTTAAAAATAAACTATGAAGATTGACTCTTTTCAGGAAAAAAGCT
 GTATATAGCACAGGGAACCCATATCTTGGGTAATCTAGTATAAAAACAAATTACTTTTAT
 TTAATTTCCCTTGTAGCAAACTAATTGCCACATGGTGCCCTATATTTTCATAGTATTTATT
 CTCTATAGTAACGTCTTAAGTGCAGCTAGCTTCTAGATTAGACTATATAGAATTTAGATAT
 TGTATTGTTCTGCTATTATAATGCTACCACATGTAGCAATAATTACAATTTTTATTAATAA
 TAAATATGTGAATATTGTTTCATGAAAGACAGATTTCCAATCTCTTCTCTCTCTGTA
 CTGCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

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FIGURE 230

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648 .
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR

Important features of the protein:**Signal peptide:**

amino acids 1-26

FIGURE 231

CGCGGCGGGGCGCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC
CATGCCGTGGCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGGCCAGACAACCCGGCCATGCT
 TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCCTGACTCGG
 GTGGATTGTAGCGGGCTGGGCCCCACATCATGCGGTGCCCATCCCTCTGGACACAGCCCA
 CTTGGACCTGTCTCCAACCGGCTGGAGATGGTGAATGAGTTCGGTGTGGCGGGGCGGGCT
 ACACGACGTTGGCTGGCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCAACCATGCC
 TTCTCCCGCCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC
 AGCCGAGAGCTTCACCAGCTCACCCCTGAGCGACGTGAACCTTAGCCACAACAGCTCCGGG
 AGGCTCAGTGTCTGCCCTCACGACGCACAGTCAGGGCCGGGCATACACGTGGACCTTCC
 CACAACCTCATTCACCGCCTCGTGCCCCACCCACGAGGGCGGGCCTGCCGTGCGCCACCAT
 TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCCAACCTCCGAGACTTGCCCC
 TGCGCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCTATTGGTCCGGGTGCCCTTCGCGGGG
 CTGGGAGGCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG
 TGGCTTCCGTGAGCTACCGGGCTGCAGGTCTTGGACCTGTCGGGCAACCCCAAGCTTAACT
 GGGCAGGAGCTGAGTGTCTTTCAGGCCGTGAGCTCCCTGCGAGGCTGGACCTTTTCGGGCACC
 AACCTGTGCGCCCTGCCGTGAGGCGCTGCTCTCCACCTCCGAGCTGCAGAGGCTCAGCT
 GGGCCAGGATGTGCGGTGCCGGCGCCTGGTGCGGGAGGGCACCTACCCCCGAGGCCTGGCT
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCGGGAATCTGCTGCCAGGGGCCCCACC
 ATCTTGT**GA**CAAAATGGTGTGGCCAGGGCCACATAACAGACTGCTGCTGGGTGCCCTCAG
 GTCGCCGTAACCTATGTCTCAATGTGCCAACACCAAGTGGGGAGCCCGCAGGCCTATGTGGCA
 GCGTCACCAAGGAGTTGTGGGCTTAGGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC
 AAAGTCTCACCCCTTTGTCTACGTTGCTTCCCCAAACCATGACAGAGGGACTTCATGGCCA
 AACCAGACTCGGGTCCCTCCTGCTTCCCTTCCCCACTTATCCCCCAAGTCCCTTCCCTCAT
 GCCTGGGCCGGCTGACCCGCAATGGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGGCAGA
 GTTCAGGTCACCTGGGCTGAGTGTCCCTTGGGCCCATGGCCAGTCACCTCAGGGGCGAGTT
 TCTTTTCTAACATAGCCCTTTCTTTGGCATGAGGCCATGAGGCCCGCTTCATCCTTTTCTAT
 TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCCTTCTCATGTGAC
 AGATGGGGAACCTGAGGCCCTTGAAGAAGAAAAGGCTAATCTAAGTTCCCTGCGGGCAGTGGC
 ATGACTGGAGCACAGCCTCCTGCCTCCAGCCCGGACCCCAATGCACTTTCTTGTCTCCTCTA
 ATAAGCCCCACCTCCCGCCTGGGCTCCCTTGCTGCGCCTTGCTGTCCCCATTAGCACA
 GGAGTAGCAGCAGCAGCAGGCAAGAGCCTCACAAGTGGGACTCTGGGCCCTTGACCAAGT
 GTGCGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCATTTGGTT
 CCAGCCTAGCCAGTTTCTCACCTGGGTGGGGTCCCCAGCATCCAGACTGGAAACCTACC
 CATTTCCTCCTGAGCATCTCTAGATGCTGCCCAAGGAGTTGCTGCACTTTCTGGAGCCTCA
 TCTGGCTGGGATCTCAAGGGGCTCCTGGATTAGTCCCCACTGGCCCTGAGCAGCAGC
 CCTTCTTACCCTCCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCCGACCCATGCTATGTC
 TCTACCTCCAGGGCAGCATCTCAGCTTCCGAACCTGGGCTGTTTCTTGTCTTCATTTTA
 TAAAGTTGTGCTTTTAAACGAGTGTCACTTTCAACCGGCTCCCTACCCCTGCTGGC
 CGGGGATGGAGACATGTCATTTGTAAAGCAGAAAAGGTTGCACTTTGTTCATTTTGTAAAT
 ATTGTCCTGGGCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC
 AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGCTTCCCCACCTGGCTAGC
 CCATCACTATCTAAACCGTCTTGATTTAATAAACACTATAAAAGGTTTAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 232

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLLAVSGAQTTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPTRAGLPPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAAGLGLTHLSLASLQRLPELAPS
GFRELPGQLVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRSAARGPTIL
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Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGG
 GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATCCCCA
 AAACAAGTTTTGACATTCCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT
 GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
 CACGACCTGTGCCACCACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCAC
 GGGAGGCTTGGCAGTTTTTCTTACTCTGTGGTCTCCAGATTTACGGCCTAAGATGAAAGCC
 TCTAGTCTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT
 GCTAAGACTCTATCTGGACAGGGTATTTAAAAACTACCAGACCCTGACCATTATACTCTCC
 GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
 CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTAGACATTCTTC
 TGCAATGGATGGAGGAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGT
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT
 GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCAATGAT
 TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGATAAGATTTTGTGAATATCTT
 TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTGTCTATTTAATGTATTT
 ATTTTTTTACTTGGACATGAAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG
 AGCAGGTGATGATTTTTATACAGTAAAAAAAAAAACCTTGTAATTTCTAGAAGAGTGGCT
 AGGGGGGTATTCAATTGTATTCAACTAAGGACATATTACTCATGCTGATGCTCTGTGAGA
 TATTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATT
 GACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT
 CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTCTACAAATAAAGTTTTCTTTGCATA
 CCAAAAAAAAAAAAAAAAAA

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FIGURE 234

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNGKATTCATNSHSDSELRP
EIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSEFLTICKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG
ELDILLQWMEETE

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

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FIGURE 235

CCGTTATCGTCTTGCGCTACTGCTGA**ATG**TCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCG
 CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC
 CGAGCTAGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG
 CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
 GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT
 TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG
 TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATG
 GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAAC TGACCTAGTGAAGGTT CAGATGCAAAT
 GGAAGGAAAAAGGAAACTGGAAGGAAAACCATTGCGATTTCGTGGTG TACATCATGCATTTG
 CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA
 AGAGCAGCACTGGTGAATATGGGAGATTTAACCACTTATGATACAGTGAACACTACTTGGT
 ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC
 TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCA
 CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATT CAGGCTGT
 TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTACCATCTTGGCTGAGAATGACCC
 CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
 TTTT**TAA**

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FIGURE 236

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGA
RESAPYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFGESEDEH
YPLWKSIVIGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVNLTPLEDNIMTHGLSSLCSGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFPLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF
```

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC
GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTAAATGAAAAATTTATGC
TTAAGAAGTAAAAATGGCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG
ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCGCAGGTATATTGTTTTTACAGGC
TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT
TCACACATGTGGTGATTTTCCACATTGGCTTCTTCATGATAAATGCTGTATCCAATGCTC
AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTAGGAAGAACAGGTGCTCGAGTTGGCTT
TTCATTGGTTTCATGTTGATGTTTGGGTCACCTATTGCTTCCATGTGGATTCTTTTTGGTGC
ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACCTTA
TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC
TTCTTAAGTCACATTTTCCTTTTGTTATATTCTGTTTGATAGATAGGTTTTTATCTCTCAGT
ACACATTGCCAAATGGAGTAGATTGTACATTAATGTTTTGTTTCTTACATTTTTATGTTC
TGAGTTTGAAGTAGTTTTATGAAATTTCTTTATTTTTCATTGCATAGACTGTTAATATGTA
TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATCTCGAGATTTAGAA
CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT
CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAGGCCGAGCGGG
CCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCATCTACT
AAAAATACAAAAATAGCCAGGCATGGTGGTGGGTGCTGTAATCCAGCTACCTGGGAGGC
TGAGGCAGGAGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC
TGCACCTAGCCTGGGGGAGAAAGTGAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC
TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA
TAAAGGTTTTTCAGCAAGTTGTAACCTATTTTGCCCTAAAAATGAGGTTTTTTTGGTAAAGA
AAAAATATTGTTCTTATGTATTGAAGAAGGTACTTTTATATAATGATTTTTTAAATGCC
AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTTATGTGAGAA

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FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWWMIDAADVYPKPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFGRTTELWT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 239

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
 CTGGCGGCCCGCAACACTCCGTCTCACCTCTGGGCCACTGCATCTAGAGGAGGGCCGTCT
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGT
 GGTCACTGGGTGAGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGAAGCTGACCCCAAGCCACCCTTACCTGGACAG
GATGAGAGTGTGAGGTGTGCTTCGCCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA
 TGTTTATTCTGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
 GCCTCGCCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC
 AGCCAACTACTTTGCGTTTAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT
 GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCATAACATC
 GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG
 AGATGTTATGCACCTAGTGAAATTCTTAAAGAAATTCGGGGGGTGCAGTGGTGTCTGGTG
 CCTCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAACTCTTCTGACTTG
 GGGAGTTCTTACGAAAAACAACCTGGGCTTCCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA
 CCTCAGGGGTAAAAGCCCCCTTTGAGCAGTTCTTAAAGAACAGCCAGACACAAACAAATACG
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTAGGGTGGC
 TGTGGCTCTTCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG
 GCAGGGGCTGAGGAGGAGAGCAGGGGTGCTGCGTGGAAGGTGCTGCAGGTCTTGCACGC
 TGTGTCGCGCTCTCCTCCTCGGAAACAGAACCTCCACAGCACATCTACCCGGAAGACC
 AGCCTCAGAGGGTCCTTCTGGAACAGCTGTCTGTGGAGAGAATGGGTGCTTTTCGTACGGG
 ACTGCTGACGGCTGGTCTGAGGAAGGACAACTGCCAGACTTGAGCCCAATTAAATTTTA
 TTTTGTCTGTTTGAIAAAAAAAAAAAAAAAAAA

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FIGURE 240

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
 ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
 DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRLFSDLGSSYAKQLGFRDSWVFIGAKD
 LRGKSPFEQFLKNSPDTNKYEGWPPELMEGCMPPKPF

Important features:

Signal peptide:

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTGTCTCTGGGGAT
 CCAGAAACCCATGATACCTACTGAACACCGAATCCCTGGAAGCCACAGAGACAGAGACA
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC
 TCACTCCTCCCTCCCTCTCTCTGCTGTCTTAGTCTCTAGTCTCAAATCCCAGTCCC
 CTGCACCCCTTCTCTGGGACACTATGTTCTCCGCCCTCTGCTGGAGGTGATTGGATCC
 TGGCTCGAGATGGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCA
 GCCTCTTACCTGAGTGTGAAACAATGCCAGTCGCCCATCGATATTCAGACAGACAGTGT
 GACATTTGACCCTGATTTGCTGTCTGCAGCCCCACGGATATGACCAGCCTGGCACCAGGC
 CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCCCTACCCTGTATCTG
 GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACCTGGGGTCAGAAAGGATC
 CCCAGGGGGGTGAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC
 ATTATGACTCTGATTCCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCCTCAGGGCTGGCT
 GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
 TCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTCAACCTAAGAG
 AGCTGCTCCCCAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT
 TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT
 GGAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGCTCTTTGCTTCTTTTCATCCAAGCAGGA
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG
 CCTTCTCTGGCTGTTTATTTTCATTGCTAGAAAGATTGGAAGAAGAGGCTGGAAAACCGAA
 AGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCA
 TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAATGGGGTGTAGGATCTG
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCTCCTTCCCTGGACATCTCTTAGAGAG
 GAATGGAGCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTCAGCCTTCCAAACATGTA
 GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAATCTGTTTAGTTGCGAGG
 GAAGTTTGGGATATACCCCAAAGTCTCTACCCCTCACTTTTATGGCCCTTTCCCTAGATA
 TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTGTATCAATA
 TATTTGAAATTAAGTTCTGACTTT

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FIGURE 242

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWFPASYPECGNAQSPIDIQTDSVTFDPDLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKSGGSEHQ
INSEATFAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNRLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGT
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKS VVFTSAQATTEA

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

[illegible]

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FIGURE 244

MRSTILLFCLLGSTRSLPQLKPAIGLPPTKLPDQGTLPNQQQSNQVFPSLSLIPLTQM
 LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPPIFVTQLGAQGTILSSEE
 LPQIFTSLIIHSLFPGGILPFSQAGANPDVQDGSLPAGGAGVNPATQGTTPAGRLPTPSG
 TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:
 amino acids 1-16

FIGURE 245

GGAGAGAGGCGCGCGGGTGAAGGCGCATTGATGCAGCCTGCGGCGGCCCTCGGAGCGCGGCG
 GAGCCAGACGCTGACCACGTTCTCTCTCGGTCTCTCCGCTCCAGCTCCGCGCTGCCCG
 GCAGCCGGGAGCC**ATG**CGACCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCCTCC
 TGCTGCTCTGCTGCTGCAGCTGCCCCGCGCCGTGAGCGCCTCTGAGATCCCCAAGGGGAAG
 CAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
 GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTATTCCGGGTACACCTG
 GGATCCCAGGTGCGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTTGAG
 GAGTCCTGGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT
 TGGGAAAATTGCGGAGTGACATTTACAAAGATGCGTTCA~~AA~~ATAGTGCTCTAAGAGTTTTGT
 TCAGTGGCTCACTTCGGCTAA~~AA~~ATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTC
 AATGGAGCTGAATGTTTCAGGACCTCTTCCCATGAAGCTATAATTTATTTGGACCAAGGAAG
 CCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG
 GAATTGGTGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAAA
 GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAA**TA**
AATGCTTTAATTTTTCATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCACTTAAAT
 GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA
 CCAAAGTGTGATTTCACTACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGT
 GGTTTCAATATTTTGTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA
 TAATTTGGAATATTTGTTGTGGTCTTTGTTTTTCTCTTAGTATAGCATTTTTAAAAAATA
 TAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAAT
 AAAAATTATTTCCAACA

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FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop .

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLQLPAPSSASEIPK GKQKAQLRQREVVDLYNGMCLQGPA
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAI IYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNVSRIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217